



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 10, 2025 – 12:53 PM EST

PDB ID : 4DR2
Title : Crystal structure of the *Thermus thermophilus* (HB8) 30S ribosomal subunit with multiple copies of paromomycin molecules bound
Authors : Demirci, H.; Murphy IV, F.; Murphy, E.; Gregory, S.T.; Dahlberg, A.E.; Jogl, G.
Deposited on : 2012-02-16
Resolution : 3.25 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

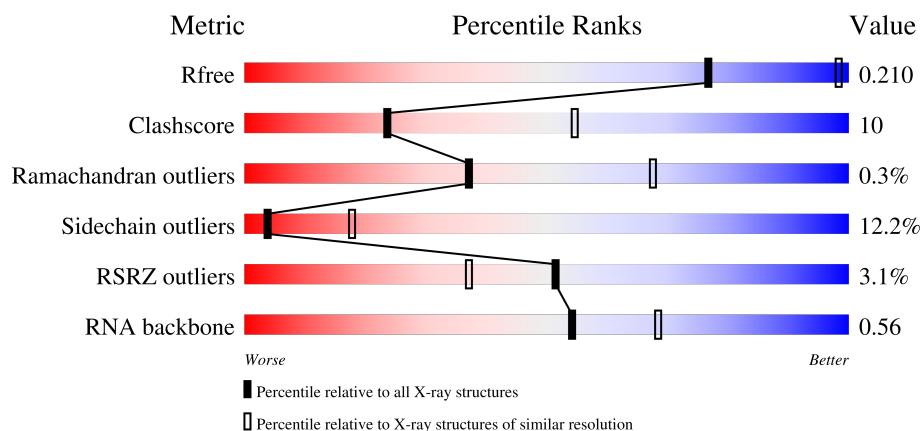
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


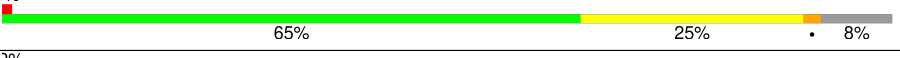

The reported resolution of this entry is 3.25 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.













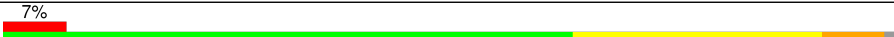


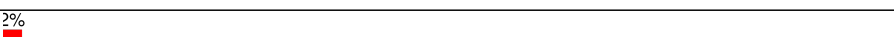
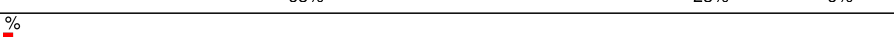
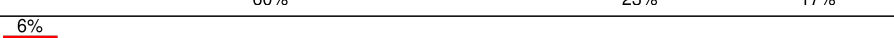

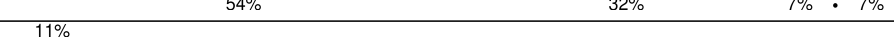
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	1999 (3.28-3.20)
Clashscore	180529	2147 (3.28-3.20)
Ramachandran outliers	177936	2118 (3.28-3.20)
Sidechain outliers	177891	2117 (3.28-3.20)
RSRZ outliers	164620	2001 (3.28-3.20)
RNA backbone	3690	1135 (3.58-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1522	
2	B	256	
3	C	239	

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Mol	Chain	Length	Quality of chain
4	D	209	
5	E	162	
6	F	101	
7	G	156	
8	H	138	
9	I	128	
10	J	105	
11	K	129	
12	L	135	
13	M	126	
14	N	61	
15	O	89	
16	P	88	
17	Q	105	
18	R	88	
19	S	93	
20	T	106	
21	U	27	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
23	MG	A	1730	-	-	-	X
23	MG	A	1804	-	-	-	X
23	MG	A	1807	-	-	-	X
23	MG	A	1819	-	-	-	X
23	MG	A	1836	-	-	-	X
23	MG	A	1838	-	-	-	X
23	MG	A	1864	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
23	MG	A	1880	-	-	-	X
23	MG	A	1882	-	-	-	X
24	ZN	D	301	-	-	-	X

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 53227 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1512	Total	C	N	O	P	0	0	0
			32504	14477	6011	10505	1511			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1534	C	A	conflict	GB M26923.1
A	1535	A	C	conflict	GB M26923.1

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	236	Total	C	N	O	S	0	0	1
			1896	1211	337	343	5			

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	207	Total	C	N	O	S	0	0	1
			1613	1016	315	281	1			

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	151	Total	C	N	O	S	0	0	1
			1147	724	218	201	4			

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	I	127	Total	C	N	O	0	0	0
			1010	639	197	174			

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	99	Total	C	N	O	S	0	0	1
			793	498	157	137	1			

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	117	Total	C	N	O	S	0	0	0
			873	543	166	161	3			

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	125	Total	C	N	O	S	0	0	1
			973	612	196	163	2			

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	118	Total	C	N	O	S	0	0	0
			937	579	193	163	2			

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	60	Total	C	N	O	S	0	0	0
			491	311	104	72	4			

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	O	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	P	84	Total	C	N	O	S	0	0	1
			701	443	140	117	1			

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	Q	101	Total	C	N	O	S	0	0	0
			838	536	157	143	2			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	96	GLN	GLU	conflict	UNP Q5SHP7

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	R	73	Total	C	N	O		0	0	0
			598	381	118	99				

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	81	Total	C	N	O	S	0	0	1
			648	414	120	112	2			

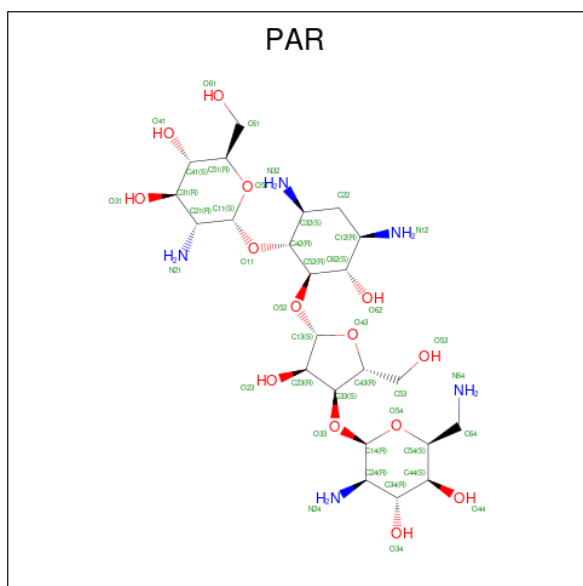
- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	T	99	Total	C	N	O	S	0	0	0
			763	470	162	129	2			

- Molecule 21 is a protein called 30S ribosomal protein THX.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	U	25	Total	C	N	O	0	0	1
			209	128	51	30			

- Molecule 22 is PAROMOMYCIN (three-letter code: PAR) (formula: $C_{23}H_{45}N_5O_{14}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
22	A	1	Total	C	N	O	0	0
			42	23	5	14		
22	A	1	Total	C	N	O	0	0
			42	23	5	14		
22	A	1	Total	C	N	O	0	0
			42	23	5	14		
22	A	1	Total	C	N	O	0	0
			42	23	5	14		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
22	A	1	Total 42	C 23	N 5	O 14	0	0
22	A	1	Total 42	C 23	N 5	O 14	0	0
22	A	1	Total 42	C 23	N 5	O 14	0	0
22	A	1	Total 42	C 23	N 5	O 14	0	0
22	A	1	Total 42	C 23	N 5	O 14	0	0
22	A	1	Total 42	C 23	N 5	O 14	0	0
22	A	1	Total 42	C 23	N 5	O 14	0	0
22	A	1	Total 42	C 23	N 5	O 14	0	0
22	A	1	Total 42	C 23	N 5	O 14	0	0
22	A	1	Total 42	C 23	N 5	O 14	0	0
22	A	1	Total 42	C 23	N 5	O 14	0	0
22	A	1	Total 42	C 23	N 5	O 14	0	0
22	A	1	Total 42	C 23	N 5	O 14	0	0
22	A	1	Total 42	C 23	N 5	O 14	0	0

- Molecule 23 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
23	A	305	Total 311	Mg 311	0	6
23	D	2	Total 2	Mg 2	0	0
23	E	2	Total 2	Mg 2	0	0
23	F	1	Total 1	Mg 1	0	0
23	H	2	Total 2	Mg 2	0	0
23	I	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
23	L	1	Total 1	Mg 1	0	0
23	N	1	Total 1	Mg 1	0	0
23	O	1	Total 1	Mg 1	0	0
23	P	1	Total 1	Mg 1	0	0
23	Q	1	Total 1	Mg 1	0	0
23	S	1	Total 1	Mg 1	0	0
23	T	2	Total 2	Mg 2	0	0

- Molecule 24 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	D	1	Total 1	Zn 1	0	0
24	N	1	Total 1	Zn 1	0	0

- Molecule 25 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	A	512	Total 512	O 512	0	0
25	C	1	Total 1	O 1	0	0
25	D	7	Total 7	O 7	0	0
25	E	6	Total 6	O 6	0	0
25	H	4	Total 4	O 4	0	0
25	L	2	Total 2	O 2	0	0
25	O	3	Total 3	O 3	0	0
25	T	1	Total 1	O 1	0	0

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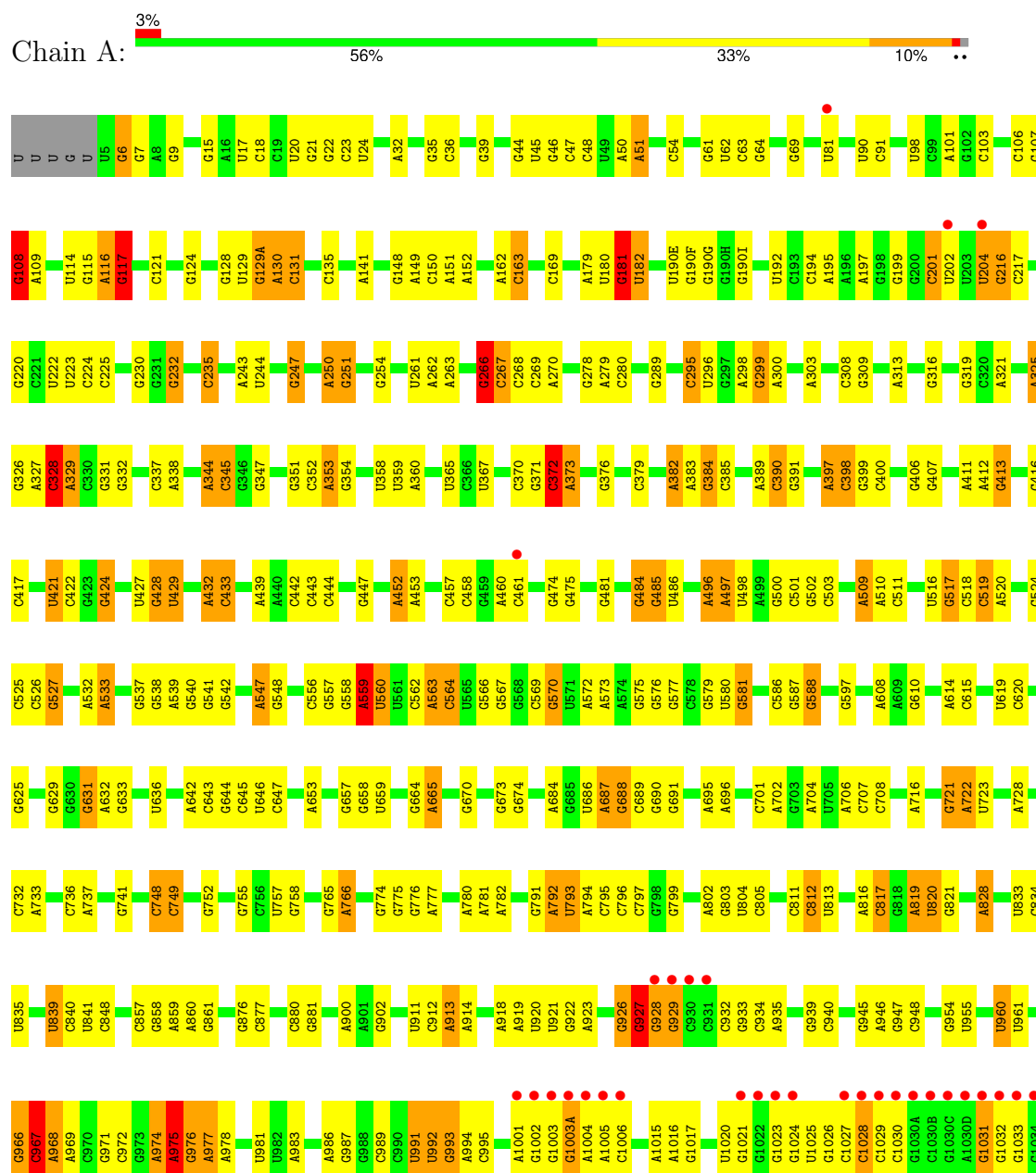
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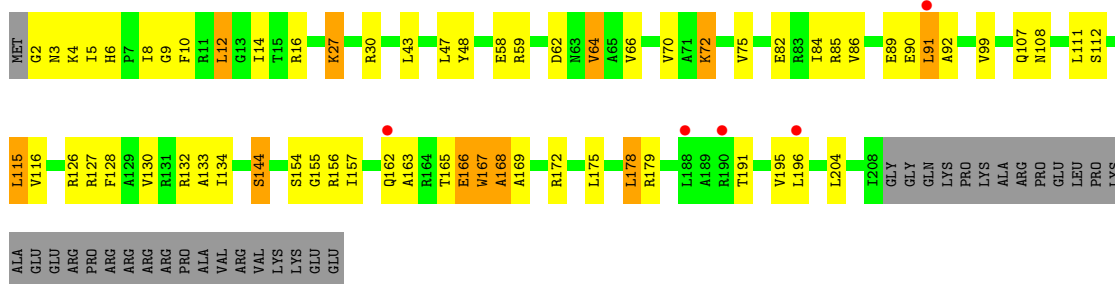
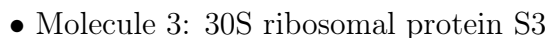
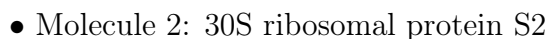
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	U	1	Total	O	0	0
			1	1		

3 Residue-property plots

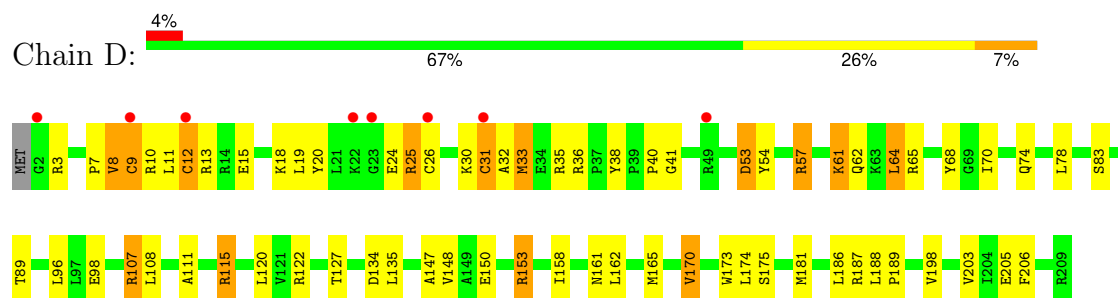
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 16S rRNA

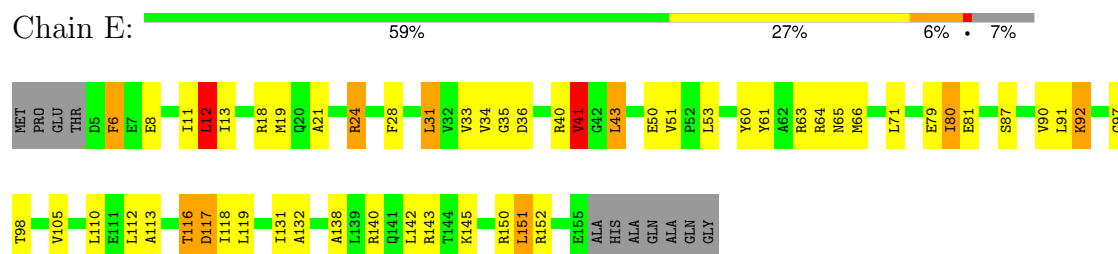




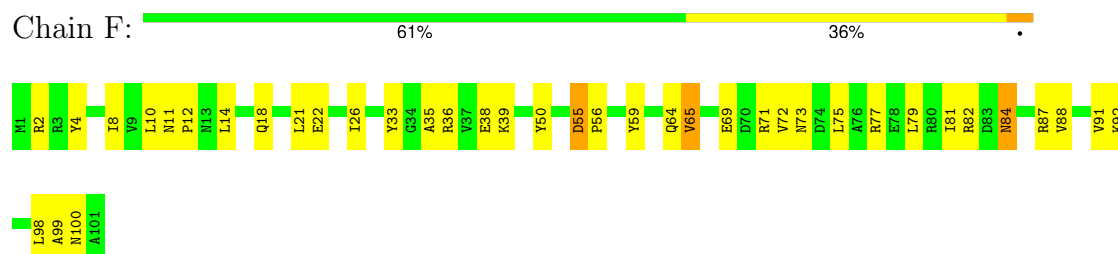
- Molecule 4: 30S ribosomal protein S4



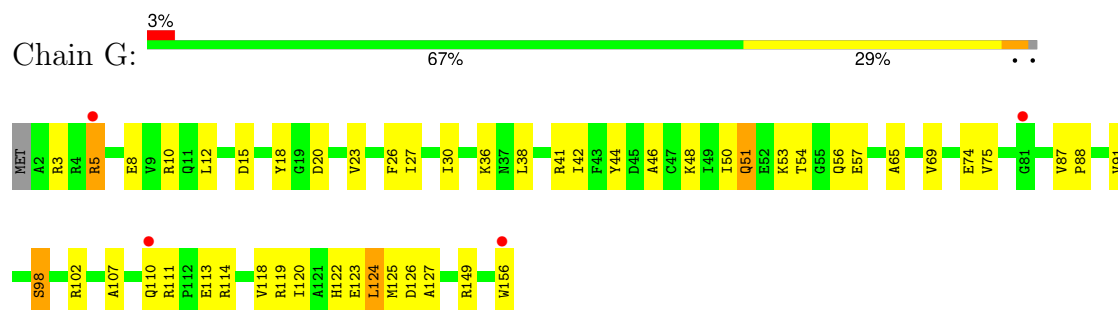
- Molecule 5: 30S ribosomal protein S5



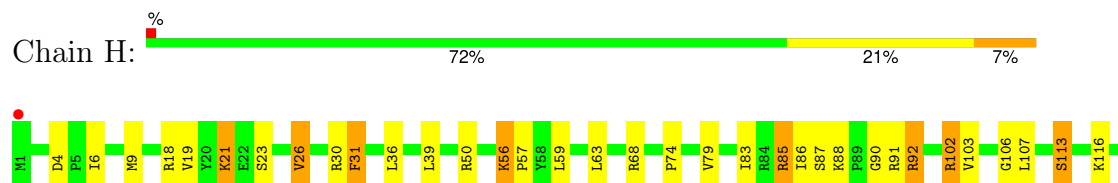
- Molecule 6: 30S ribosomal protein S6



- Molecule 7: 30S ribosomal protein S7

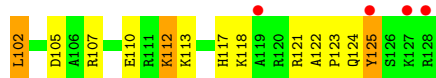


- Molecule 8: 30S ribosomal protein S8

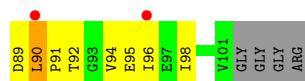
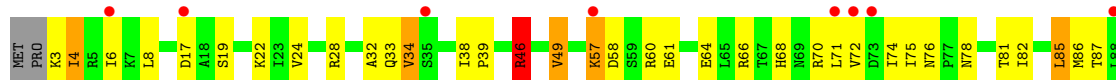




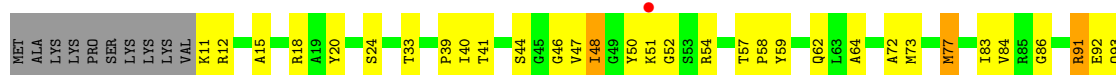
- Molecule 9: 30S ribosomal protein S9



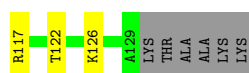
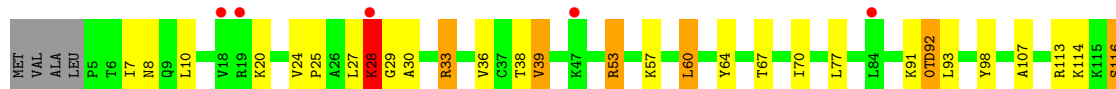
- Molecule 10: 30S ribosomal protein S10



- Molecule 11: 30S ribosomal protein S11



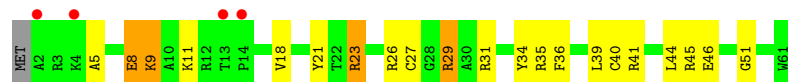
- Molecule 12: 30S ribosomal protein S12



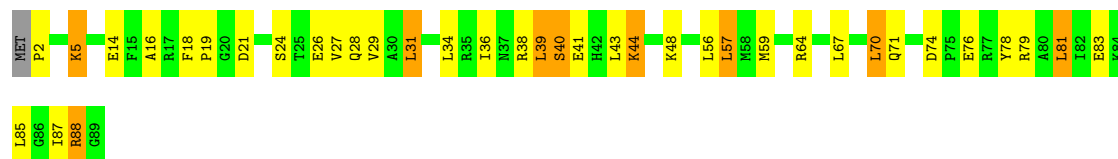
- Molecule 13: 30S ribosomal protein S13



- Molecule 14: 30S ribosomal protein S14



- Molecule 15: 30S ribosomal protein S15



- Molecule 16: 30S ribosomal protein S16



- Molecule 17: 30S ribosomal protein S17

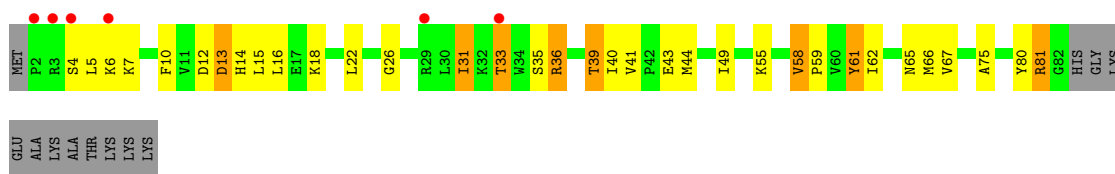


- Molecule 18: 30S ribosomal protein S18

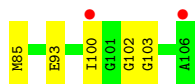


- Molecule 19: 30S ribosomal protein S19





- Molecule 20: 30S ribosomal protein S20



- Molecule 21: 30S ribosomal protein THX



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	402.60Å 402.60Å 177.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.39 – 3.25 44.39 – 3.25	Depositor EDS
% Data completeness (in resolution range)	99.6 (44.39-3.25) 99.3 (44.39-3.25)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.97 (at 3.25Å)	Xtriage
Refinement program	PHENIX dev_978	Depositor
R, R_{free}	0.171 , 0.211 0.172 , 0.210	Depositor DCC
R_{free} test set	11415 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	88.7	Xtriage
Anisotropy	0.297	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 78.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	53227	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.53% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: UR3, MA6, 5MC, PAR, MG, 4OC, 2MG, 0TD, M2G, ZN, PSU, 7MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.63	3/36037 (0.0%)	1.03	121/56239 (0.2%)
2	B	0.41	0/1931	0.65	0/2607
3	C	0.42	0/1637	0.63	0/2207
4	D	0.49	3/1733 (0.2%)	0.63	1/2318 (0.0%)
5	E	0.51	0/1163	0.75	2/1566 (0.1%)
6	F	0.37	0/856	0.59	0/1154
7	G	0.37	0/1276	0.55	0/1709
8	H	0.50	0/1136	0.71	0/1527
9	I	0.39	0/1029	0.66	0/1379
10	J	0.38	0/806	0.68	1/1084 (0.1%)
11	K	0.43	0/888	0.69	0/1198
12	L	0.49	0/978	0.70	0/1308
13	M	0.38	0/947	0.59	0/1270
14	N	0.43	0/500	0.67	0/663
15	O	0.41	0/745	0.61	0/992
16	P	0.48	0/717	0.71	0/965
17	Q	0.52	0/851	0.74	0/1136
18	R	0.40	0/604	0.60	0/801
19	S	0.34	0/662	0.61	0/892
20	T	0.48	0/765	0.70	0/1007
21	U	0.44	0/213	0.69	0/279
All	All	0.57	6/55474 (0.0%)	0.93	125/82301 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1
3	C	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
8	H	0	1
All	All	0	3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	975	A	N9-C4	-6.19	1.34	1.37
4	D	31	CYS	CB-SG	6.06	1.92	1.82
1	A	1502	A	N9-C4	-5.34	1.34	1.37
1	A	1502	A	N7-C5	-5.24	1.36	1.39
4	D	9	CYS	CB-SG	5.06	1.90	1.82

The worst 5 of 125 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	108	G	C4-C5-N7	10.01	114.81	110.80
1	A	108	G	C5-N7-C8	-9.95	99.32	104.30
1	A	1128	C	C6-N1-C2	-9.70	116.42	120.30
1	A	328	C	N1-C2-O2	9.68	124.71	118.90
1	A	1502	A	C5-N7-C8	-9.64	99.08	103.90

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	14	GLY	Peptide
3	C	166	GLU	Peptide
8	H	90	GLY	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32504	0	16434	451	0
2	B	1896	0	1936	33	0
3	C	1613	0	1677	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	1703	0	1763	50	0
5	E	1147	0	1207	35	0
6	F	843	0	857	25	0
7	G	1257	0	1296	30	0
8	H	1116	0	1177	26	0
9	I	1010	0	1037	34	0
10	J	793	0	835	33	0
11	K	873	0	894	21	0
12	L	973	0	1058	24	0
13	M	937	0	995	21	0
14	N	491	0	524	18	0
15	O	734	0	771	26	0
16	P	701	0	720	13	0
17	Q	838	0	909	22	0
18	R	598	0	670	16	0
19	S	648	0	673	20	0
20	T	763	0	861	30	0
21	U	209	0	221	6	0
22	A	714	0	765	34	0
23	A	311	0	0	0	0
23	D	2	0	0	0	0
23	E	2	0	0	0	0
23	F	1	0	0	0	0
23	H	2	0	0	0	0
23	I	1	0	0	0	0
23	L	1	0	0	0	0
23	N	1	0	0	0	0
23	O	1	0	0	0	0
23	P	1	0	0	0	0
23	Q	1	0	0	0	0
23	S	1	0	0	0	0
23	T	2	0	0	0	0
24	D	1	0	0	0	0
24	N	1	0	0	0	0
25	A	512	0	0	8	0
25	C	1	0	0	0	0
25	D	7	0	0	0	0
25	E	6	0	0	0	0
25	H	4	0	0	0	0
25	L	2	0	0	0	0
25	O	3	0	0	0	0
25	T	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	U	1	0	0	0	0
All	All	53227	0	37280	888	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 888 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:15:ALA:HA	11:K:77:MET:HA	1.51	0.90
1:A:1502:A:H2	1:A:1505:G:H1	1.15	0.89
1:A:1086:U:H3	1:A:1099:G:H22	1.23	0.86
19:S:33:THR:HG22	19:S:35:SER:H	1.41	0.85
1:A:427:U:OP1	4:D:13:ARG:NH2	2.12	0.83

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	234/256 (91%)	218 (93%)	15 (6%)	1 (0%)	30	62
3	C	205/239 (86%)	187 (91%)	16 (8%)	2 (1%)	13	44
4	D	206/209 (99%)	198 (96%)	7 (3%)	1 (0%)	25	58
5	E	149/162 (92%)	143 (96%)	6 (4%)	0	100	100
6	F	99/101 (98%)	96 (97%)	3 (3%)	0	100	100
7	G	153/156 (98%)	147 (96%)	6 (4%)	0	100	100
8	H	136/138 (99%)	134 (98%)	2 (2%)	0	100	100
9	I	125/128 (98%)	117 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	J	97/105 (92%)	82 (84%)	14 (14%)	1 (1%)	13	44
11	K	115/129 (89%)	109 (95%)	6 (5%)	0	100	100
12	L	122/135 (90%)	111 (91%)	10 (8%)	1 (1%)	16	48
13	M	116/126 (92%)	108 (93%)	8 (7%)	0	100	100
14	N	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
15	O	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
16	P	82/88 (93%)	79 (96%)	3 (4%)	0	100	100
17	Q	99/105 (94%)	94 (95%)	5 (5%)	0	100	100
18	R	71/88 (81%)	64 (90%)	7 (10%)	0	100	100
19	S	79/93 (85%)	70 (89%)	8 (10%)	1 (1%)	10	38
20	T	97/106 (92%)	88 (91%)	8 (8%)	1 (1%)	13	44
21	U	23/27 (85%)	22 (96%)	1 (4%)	0	100	100
All	All	2352/2541 (93%)	2203 (94%)	141 (6%)	8 (0%)	37	67

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	L	28	LYS
19	S	31	ILE
3	C	168	ALA
4	D	3	ARG
20	T	73	HIS

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	201/220 (91%)	177 (88%)	24 (12%)	4	18
3	C	160/188 (85%)	134 (84%)	26 (16%)	2	9
4	D	180/181 (99%)	162 (90%)	18 (10%)	6	24
5	E	115/123 (94%)	96 (84%)	19 (16%)	2	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	F	90/90 (100%)	82 (91%)	8 (9%)	8	29
7	G	126/127 (99%)	112 (89%)	14 (11%)	5	21
8	H	119/119 (100%)	103 (87%)	16 (13%)	3	14
9	I	98/99 (99%)	87 (89%)	11 (11%)	5	20
10	J	87/92 (95%)	79 (91%)	8 (9%)	7	27
11	K	89/99 (90%)	79 (89%)	10 (11%)	5	20
12	L	103/110 (94%)	92 (89%)	11 (11%)	5	22
13	M	94/101 (93%)	85 (90%)	9 (10%)	7	26
14	N	48/50 (96%)	43 (90%)	5 (10%)	5	23
15	O	79/80 (99%)	66 (84%)	13 (16%)	2	8
16	P	72/74 (97%)	64 (89%)	8 (11%)	5	21
17	Q	95/97 (98%)	84 (88%)	11 (12%)	4	19
18	R	64/77 (83%)	61 (95%)	3 (5%)	22	52
19	S	71/80 (89%)	58 (82%)	13 (18%)	1	6
20	T	76/82 (93%)	63 (83%)	13 (17%)	1	7
21	U	19/22 (86%)	17 (90%)	2 (10%)	5	23
All	All	1986/2111 (94%)	1744 (88%)	242 (12%)	4	18

5 of 242 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	H	39	LEU
19	S	36	ARG
10	J	95	GLU
19	S	15	LEU
20	T	74	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	6	HIS
3	C	108	ASN
4	D	42	GLN
6	F	73	ASN
17	Q	96	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1507/1522 (99%)	256 (16%)	35 (2%)

5 of 256 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	9	G
1	A	32	A
1	A	39	G
1	A	44	G
1	A	47	C

5 of 35 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1256	A
1	A	1281	U
1	A	1331	G
1	A	509	A
1	A	496	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

15 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	M2G	A	966	1	20,27,28	1.19	3 (15%)	19,40,43	1.28	2 (10%)
1	PSU	A	1540	1	18,21,22	1.18	1 (5%)	21,30,33	1.79	4 (19%)
1	PSU	A	1541	1,23	18,21,22	1.22	1 (5%)	21,30,33	1.80	4 (19%)
1	PSU	A	516	1,23	18,21,22	1.17	1 (5%)	21,30,33	2.02	6 (28%)
1	UR3	A	1498	1	19,22,23	1.01	1 (5%)	26,32,35	1.04	1 (3%)
1	5MC	A	1404	1	19,22,23	1.22	2 (10%)	26,32,35	0.84	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	2MG	A	1207	1	18,26,27	1.59	4 (22%)	16,38,41	1.34	2 (12%)
1	5MC	A	1400	1	19,22,23	1.29	2 (10%)	26,32,35	0.98	1 (3%)
1	MA6	A	1519	1	19,26,27	0.76	0	18,38,41	0.99	1 (5%)
1	MA6	A	1518	1	19,26,27	1.14	2 (10%)	18,38,41	0.86	1 (5%)
12	0TD	L	92	12	8,9,10	1.71	1 (12%)	6,11,13	3.11	1 (16%)
1	5MC	A	1407	1	19,22,23	0.94	0	26,32,35	0.85	1 (3%)
1	5MC	A	967	1	19,22,23	0.87	1 (5%)	26,32,35	0.87	2 (7%)
1	4OC	A	1402	1	20,23,24	1.11	3 (15%)	25,32,35	0.78	1 (4%)
1	7MG	A	527	1,23	23,26,27	4.01	4 (17%)	27,39,42	2.21	9 (33%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	M2G	A	966	1	-	1/7/29/30	0/3/3/3
1	PSU	A	1540	1	-	2/7/25/26	0/2/2/2
1	PSU	A	1541	1,23	-	1/7/25/26	0/2/2/2
1	PSU	A	516	1,23	-	0/7/25/26	0/2/2/2
1	UR3	A	1498	1	-	0/7/25/26	0/2/2/2
1	5MC	A	1404	1	-	0/7/25/26	0/2/2/2
1	2MG	A	1207	1	-	0/5/27/28	0/3/3/3
1	5MC	A	1400	1	-	2/7/25/26	0/2/2/2
1	MA6	A	1519	1	-	1/7/29/30	0/3/3/3
1	MA6	A	1518	1	-	0/7/29/30	0/3/3/3
12	0TD	L	92	12	-	2/7/12/14	-
1	5MC	A	1407	1	-	0/7/25/26	0/2/2/2
1	5MC	A	967	1	-	2/7/25/26	0/2/2/2
1	4OC	A	1402	1	-	2/9/29/30	0/2/2/2
1	7MG	A	527	1,23	-	2/7/37/38	0/3/3/3

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	527	7MG	C8-N9	-17.70	1.34	1.45
1	A	1541	PSU	C6-C5	4.20	1.39	1.35
1	A	527	7MG	C2-N2	4.04	1.43	1.34
1	A	1540	PSU	C6-C5	4.04	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	527	7MG	C4-N3	3.98	1.43	1.34

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	L	92	0TD	CSB-SB-CB	-7.34	89.17	102.36
1	A	516	PSU	N1-C2-N3	5.38	120.85	115.17
1	A	527	7MG	C5-C6-N1	5.36	120.38	110.94
1	A	527	7MG	N9-C4-N3	4.79	132.48	125.46
1	A	1540	PSU	C4-N3-C2	-4.65	119.96	126.37

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	527	7MG	O4'-C4'-C5'-O5'
1	A	1400	5MC	O4'-C4'-C5'-O5'
12	L	92	0TD	SB-CB-CG-OD2
1	A	527	7MG	C3'-C4'-C5'-O5'
1	A	967	5MC	O4'-C4'-C5'-O5'

There are no ring outliers.

8 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1498	UR3	4	0
1	A	1207	2MG	2	0
1	A	1400	5MC	1	0
1	A	1519	MA6	1	0
1	A	1518	MA6	2	0
12	L	92	0TD	2	0
1	A	967	5MC	1	0
1	A	1402	4OC	3	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 346 ligands modelled in this entry, 329 are monoatomic - leaving 17 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	PAR	A	1615	-	44,45,45	1.51	7 (15%)	63,67,67	1.63	13 (20%)
22	PAR	A	1602	-	44,45,45	1.04	3 (6%)	63,67,67	1.76	12 (19%)
22	PAR	A	1606	-	44,45,45	1.24	5 (11%)	63,67,67	1.58	16 (25%)
22	PAR	A	1613	-	44,45,45	1.67	10 (22%)	63,67,67	1.68	12 (19%)
22	PAR	A	1614	-	44,45,45	1.50	10 (22%)	63,67,67	1.66	12 (19%)
22	PAR	A	1609	-	44,45,45	1.16	5 (11%)	63,67,67	1.56	13 (20%)
22	PAR	A	1617	-	44,45,45	1.33	5 (11%)	63,67,67	1.65	12 (19%)
22	PAR	A	1604	-	44,45,45	1.18	2 (4%)	63,67,67	1.62	12 (19%)
22	PAR	A	1601	-	44,45,45	1.02	4 (9%)	63,67,67	1.51	11 (17%)
22	PAR	A	1605	-	44,45,45	1.17	3 (6%)	63,67,67	1.69	12 (19%)
22	PAR	A	1612	-	44,45,45	1.55	7 (15%)	63,67,67	1.74	11 (17%)
22	PAR	A	1616	-	44,45,45	1.36	5 (11%)	63,67,67	1.64	11 (17%)
22	PAR	A	1611	-	44,45,45	1.91	11 (25%)	63,67,67	1.62	9 (14%)
22	PAR	A	1607	-	44,45,45	1.26	4 (9%)	63,67,67	1.64	12 (19%)
22	PAR	A	1608	-	44,45,45	1.15	3 (6%)	63,67,67	1.68	12 (19%)
22	PAR	A	1610	-	44,45,45	1.58	7 (15%)	63,67,67	1.71	11 (17%)
22	PAR	A	1603	-	44,45,45	1.32	3 (6%)	63,67,67	1.55	9 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	PAR	A	1615	-	-	11/18/94/94	1/4/4/4
22	PAR	A	1602	-	-	7/18/94/94	0/4/4/4
22	PAR	A	1606	-	-	7/18/94/94	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	PAR	A	1613	-	-	11/18/94/94	0/4/4/4
22	PAR	A	1614	-	-	5/18/94/94	0/4/4/4
22	PAR	A	1609	-	-	2/18/94/94	0/4/4/4
22	PAR	A	1617	-	-	3/18/94/94	1/4/4/4
22	PAR	A	1604	-	-	6/18/94/94	0/4/4/4
22	PAR	A	1601	-	-	4/18/94/94	0/4/4/4
22	PAR	A	1605	-	-	3/18/94/94	0/4/4/4
22	PAR	A	1612	-	-	8/18/94/94	0/4/4/4
22	PAR	A	1616	-	-	9/18/94/94	1/4/4/4
22	PAR	A	1611	-	-	7/18/94/94	0/4/4/4
22	PAR	A	1607	-	-	4/18/94/94	0/4/4/4
22	PAR	A	1608	-	-	8/18/94/94	0/4/4/4
22	PAR	A	1610	-	-	7/18/94/94	0/4/4/4
22	PAR	A	1603	-	-	3/18/94/94	0/4/4/4

The worst 5 of 94 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	A	1611	PAR	C13-C23	5.17	1.59	1.52
22	A	1611	PAR	C52-C42	4.90	1.62	1.52
22	A	1603	PAR	C31-C21	4.79	1.59	1.53
22	A	1615	PAR	C34-C24	4.57	1.59	1.53
22	A	1612	PAR	C14-C24	4.36	1.60	1.52

The worst 5 of 200 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	A	1612	PAR	O33-C14-C24	7.86	120.94	108.08
22	A	1610	PAR	O33-C14-C24	7.53	120.40	108.08
22	A	1602	PAR	O33-C14-C24	7.26	119.96	108.08
22	A	1611	PAR	O33-C14-C24	6.96	119.46	108.08
22	A	1605	PAR	O33-C14-C24	6.92	119.40	108.08

There are no chirality outliers.

5 of 105 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
22	A	1602	PAR	C23-C13-O52-C52

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Mol	Chain	Res	Type	Atoms
22	A	1602	PAR	O43-C13-O52-C52
22	A	1602	PAR	C24-C14-O33-C33
22	A	1602	PAR	O54-C54-C64-N64
22	A	1604	PAR	C23-C13-O52-C52

All (3) ring outliers are listed below:

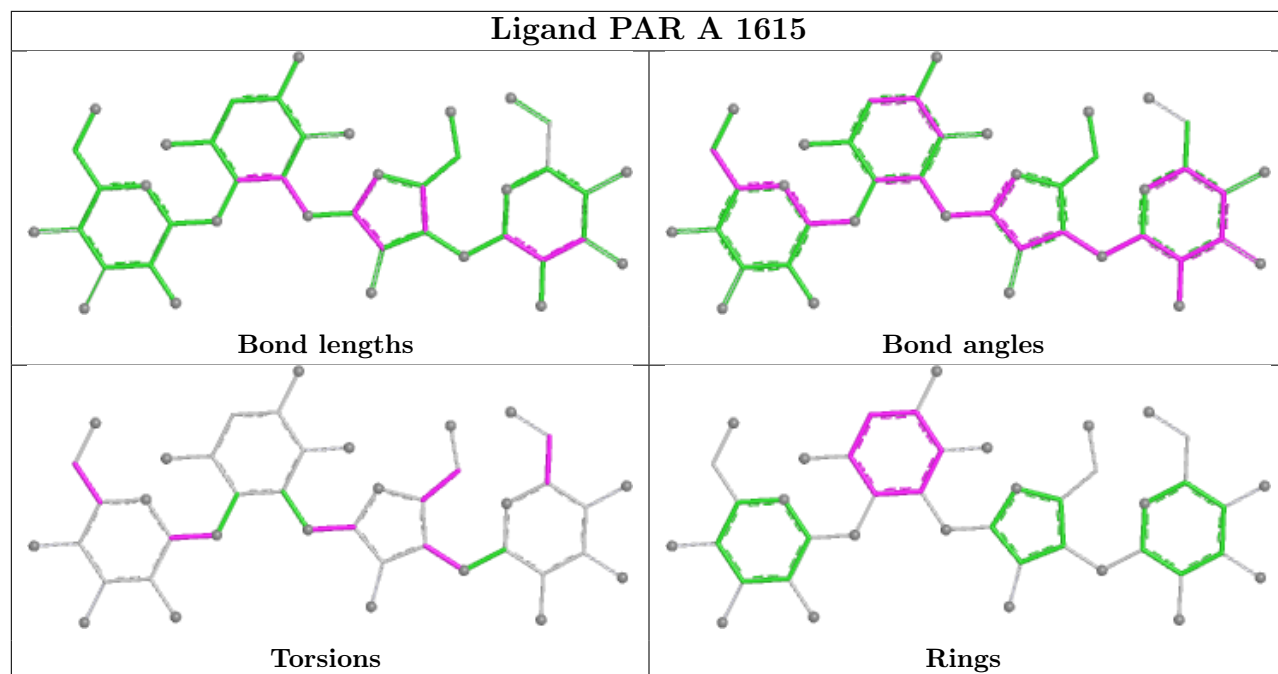
Mol	Chain	Res	Type	Atoms
22	A	1616	PAR	C12-C22-C32-C42-C52-C62
22	A	1615	PAR	C12-C22-C32-C42-C52-C62
22	A	1617	PAR	C12-C22-C32-C42-C52-C62

15 monomers are involved in 34 short contacts:

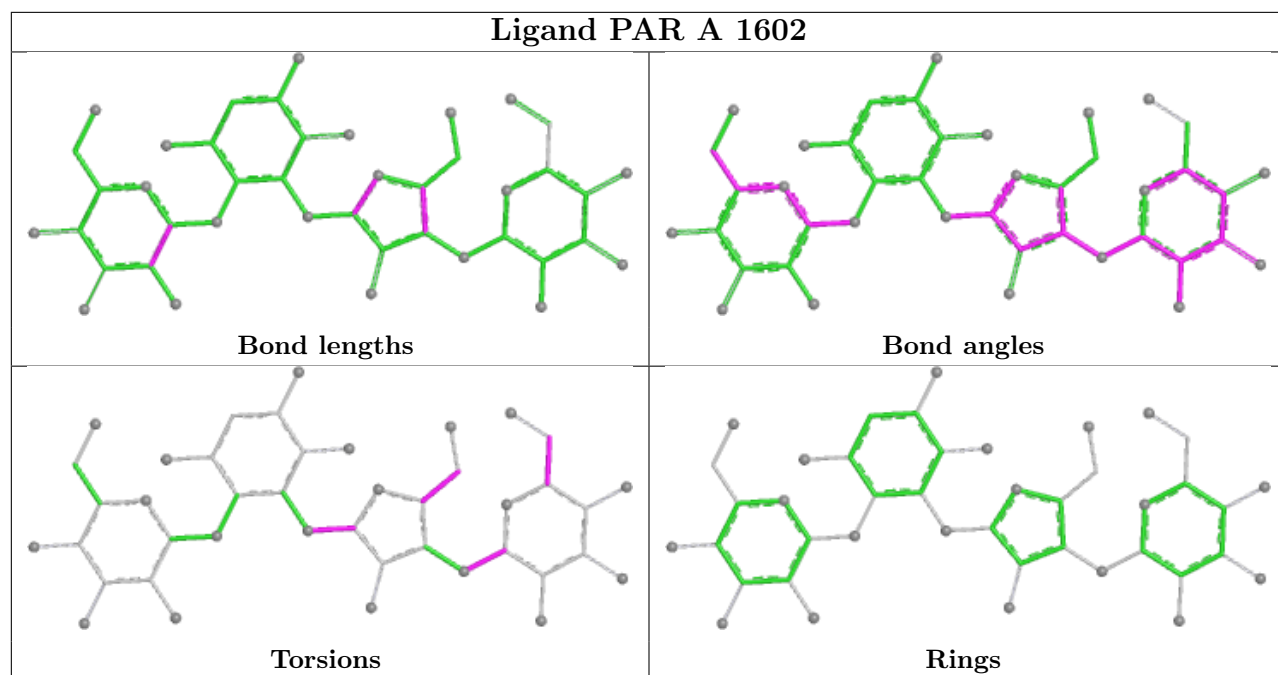
Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	A	1615	PAR	1	0
22	A	1602	PAR	1	0
22	A	1606	PAR	2	0
22	A	1613	PAR	6	0
22	A	1614	PAR	3	0
22	A	1609	PAR	1	0
22	A	1617	PAR	2	0
22	A	1604	PAR	3	0
22	A	1601	PAR	1	0
22	A	1612	PAR	4	0
22	A	1616	PAR	3	0
22	A	1611	PAR	1	0
22	A	1607	PAR	2	0
22	A	1608	PAR	1	0
22	A	1610	PAR	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

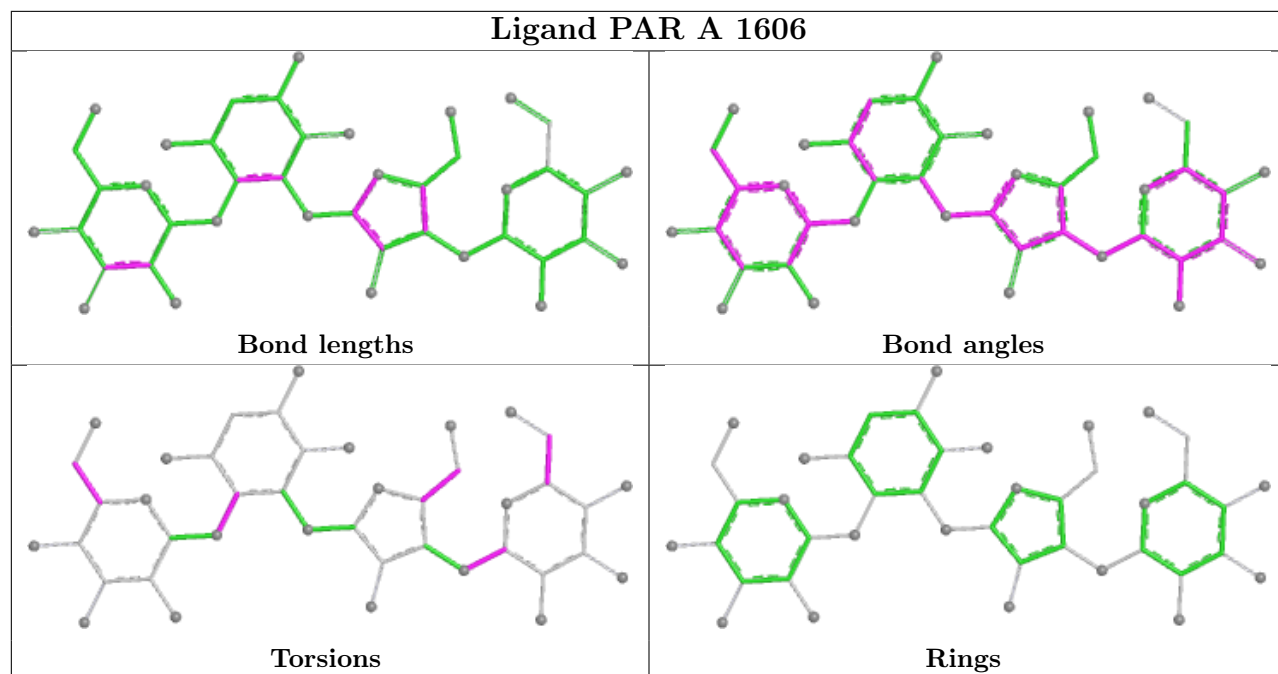
Ligand PAR A 1615



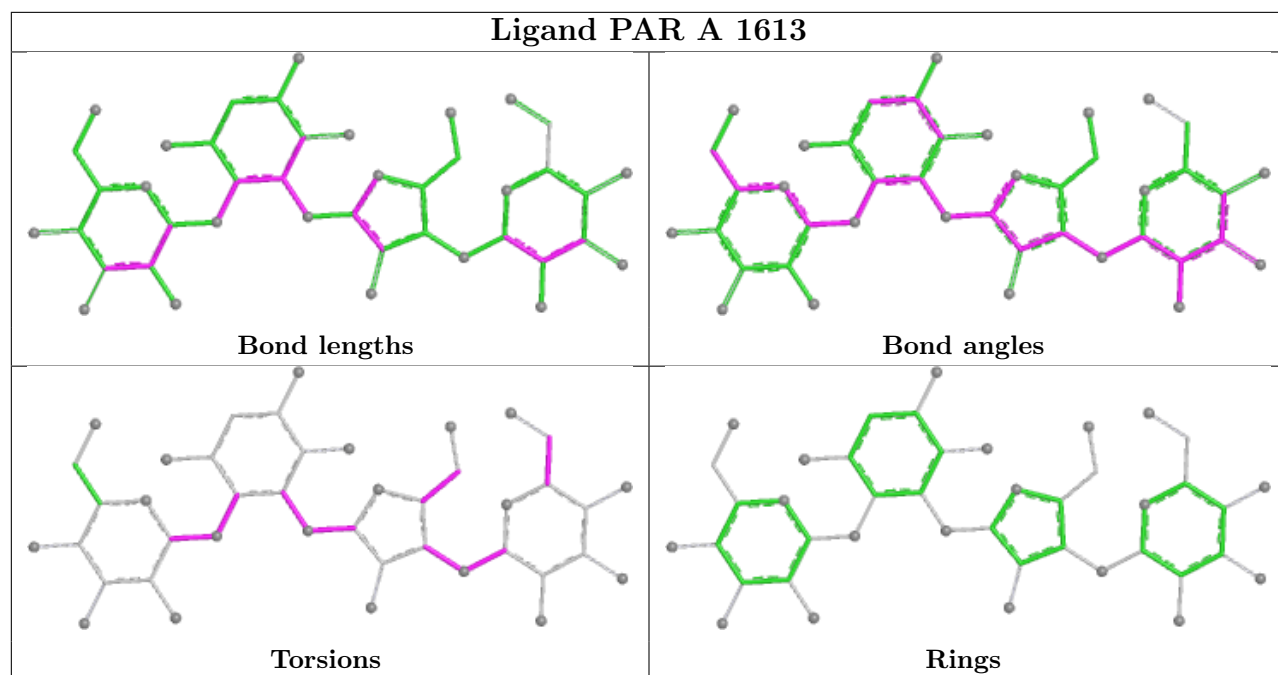
Ligand PAR A 1602



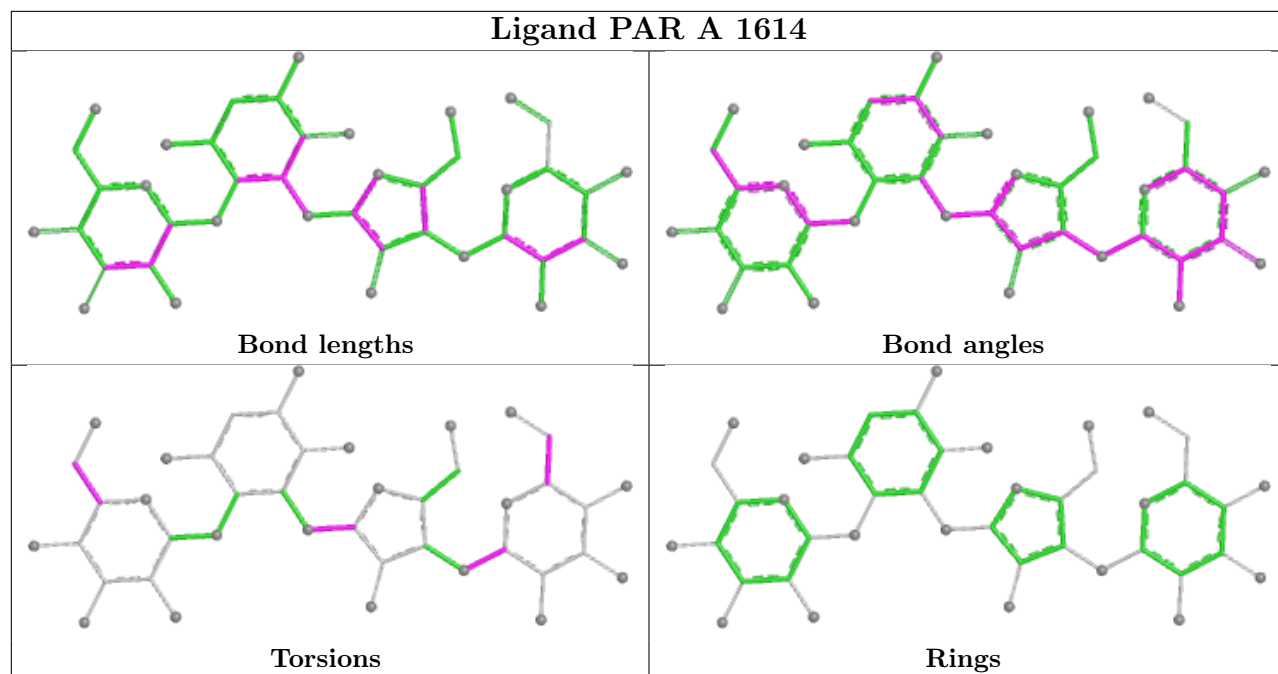
Ligand PAR A 1606



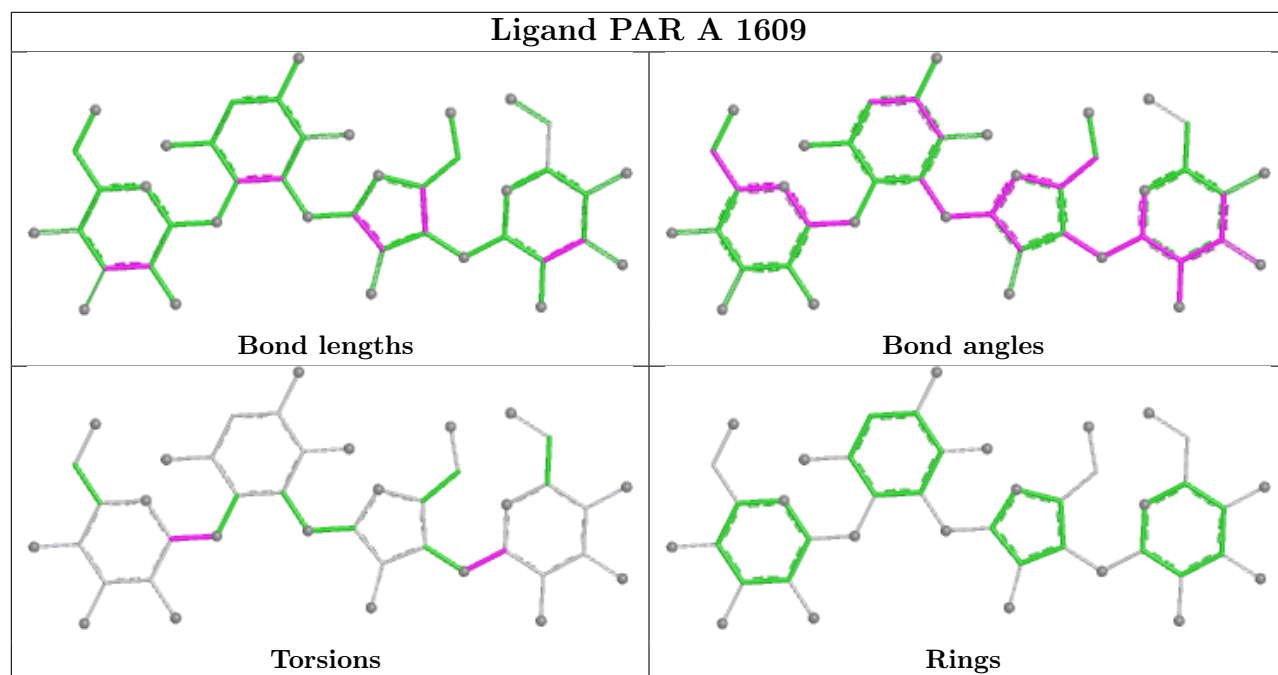
Ligand PAR A 1613



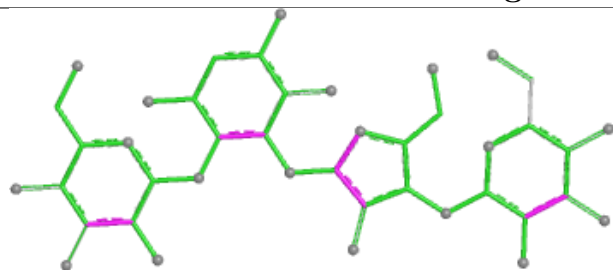
Ligand PAR A 1614



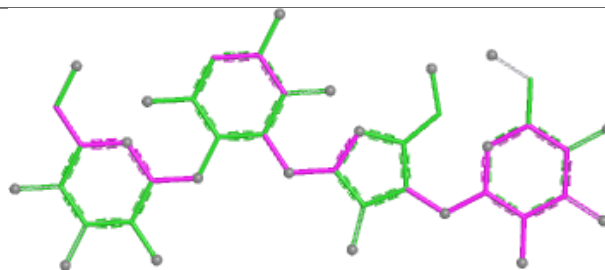
Ligand PAR A 1609



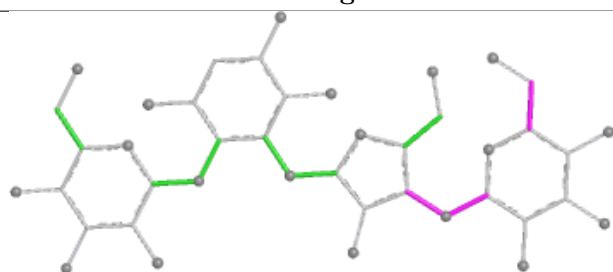
Ligand PAR A 1617



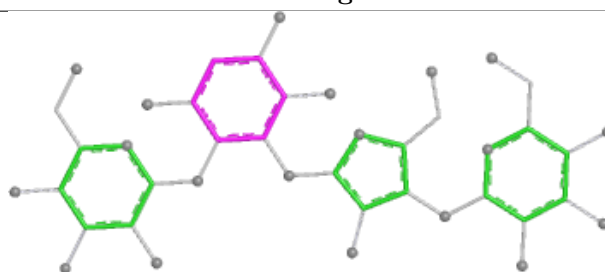
Bond lengths



Bond angles

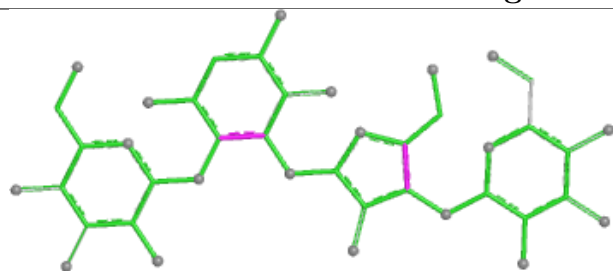


Torsions

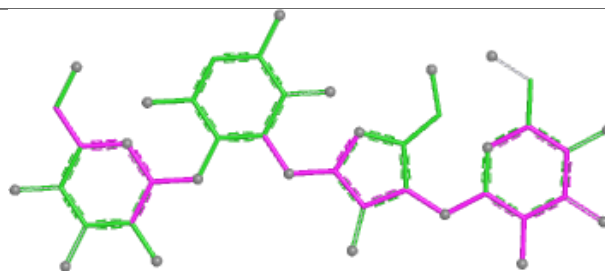


Rings

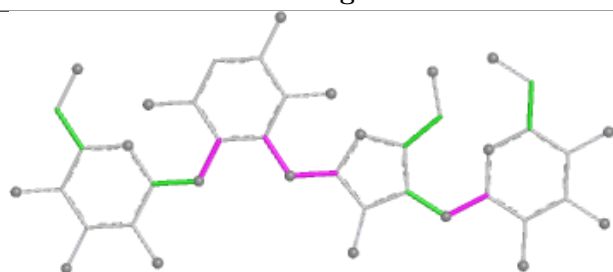
Ligand PAR A 1604



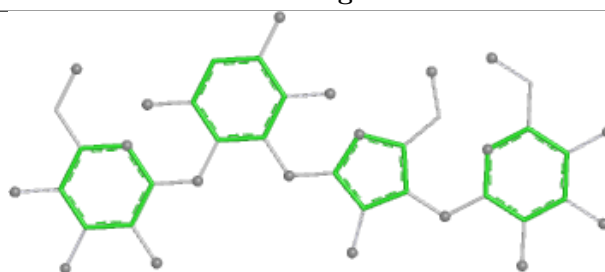
Bond lengths



Bond angles

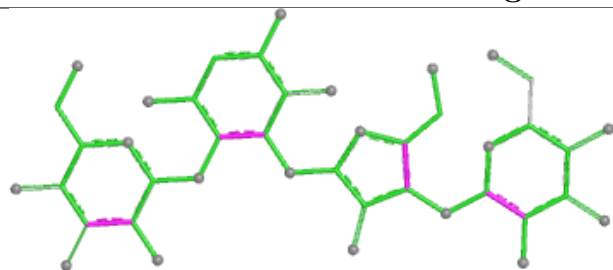


Torsions

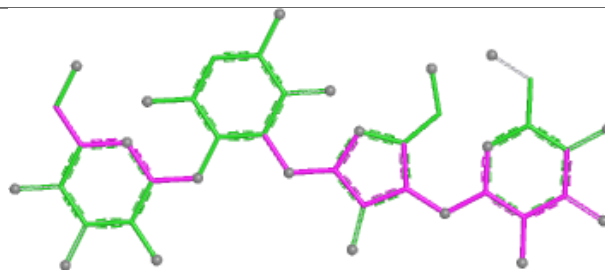


Rings

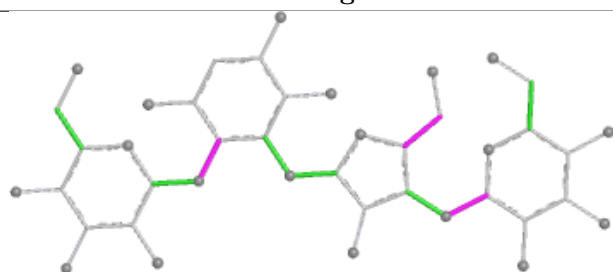
Ligand PAR A 1601



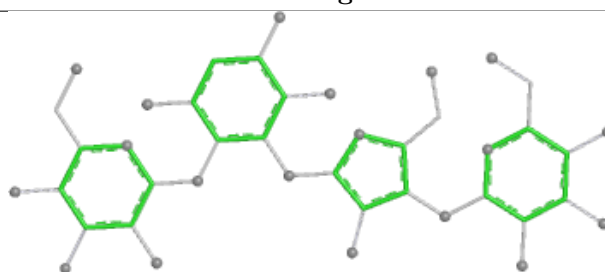
Bond lengths



Bond angles

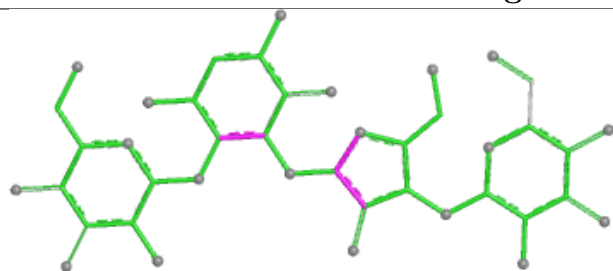


Torsions

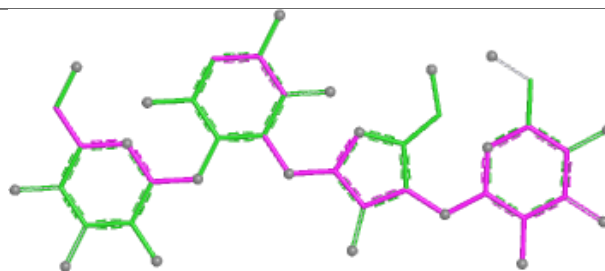


Rings

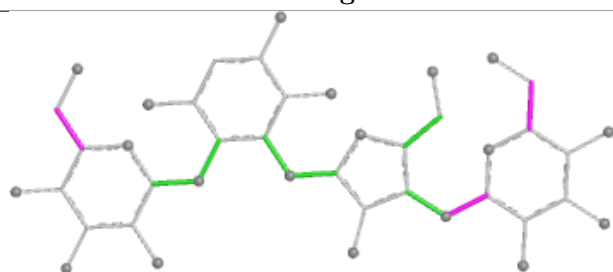
Ligand PAR A 1605



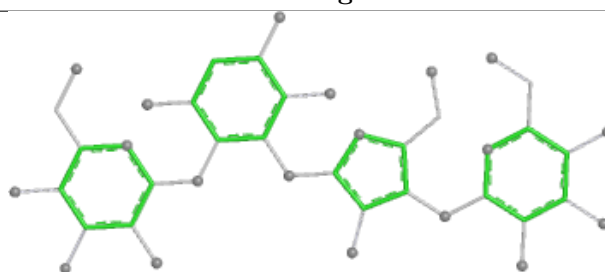
Bond lengths



Bond angles

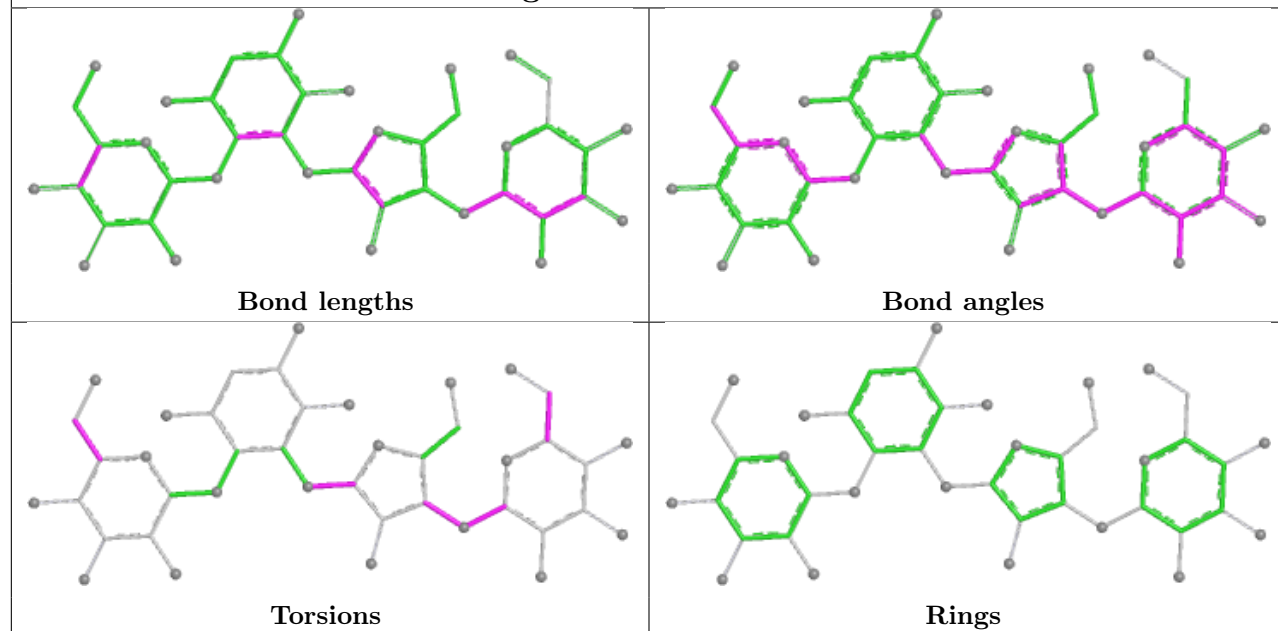


Torsions

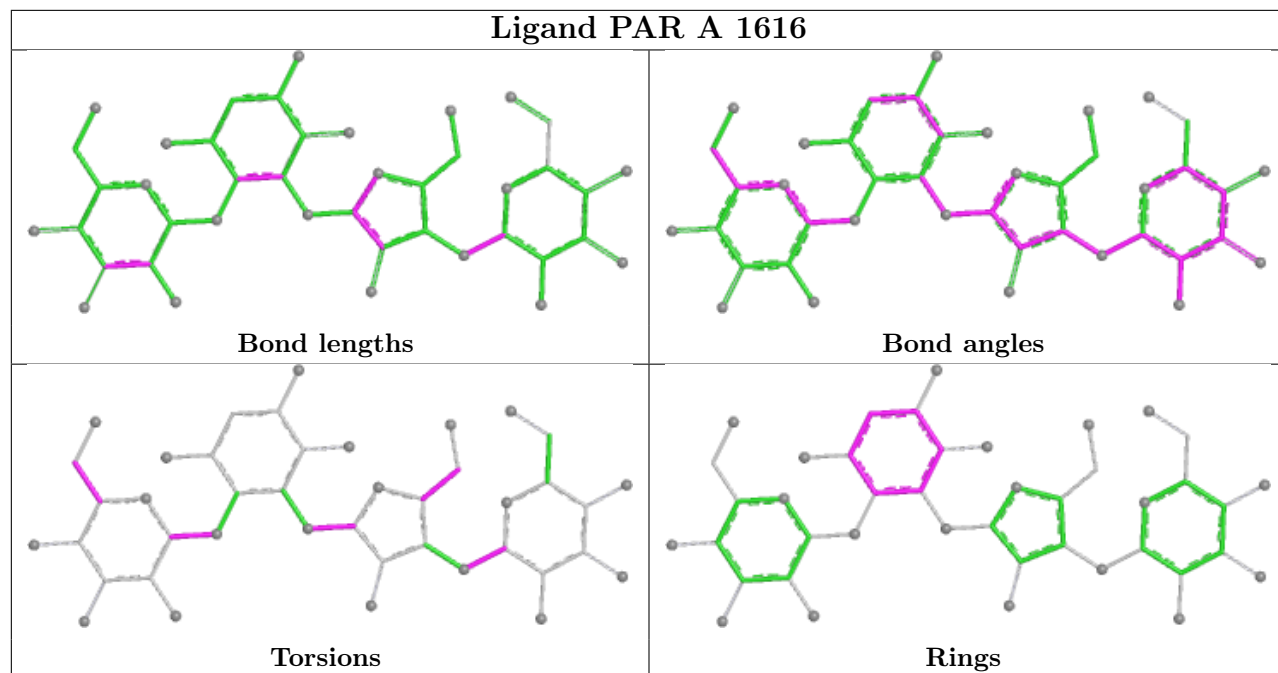


Rings

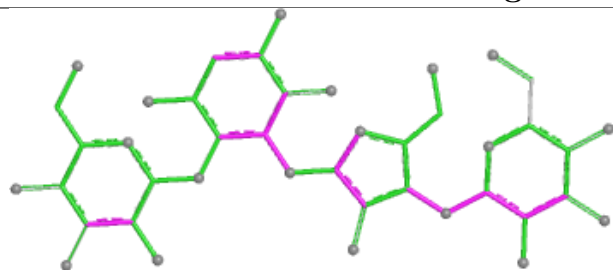
Ligand PAR A 1612



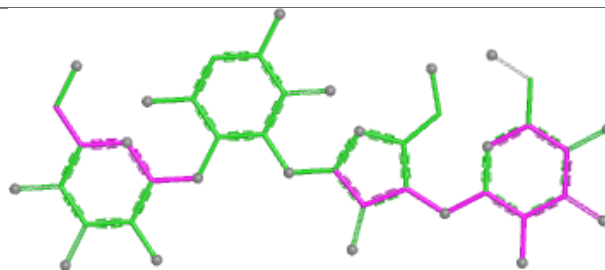
Ligand PAR A 1616



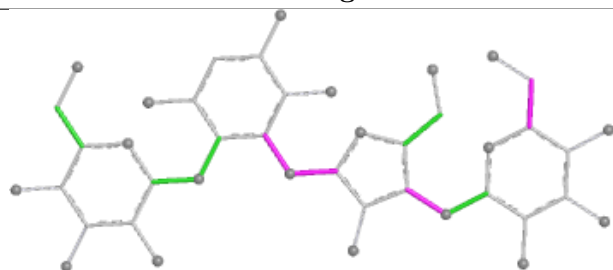
Ligand PAR A 1611



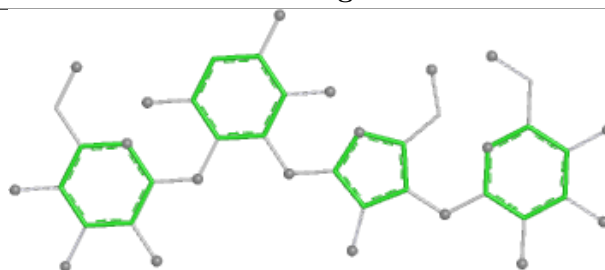
Bond lengths



Bond angles

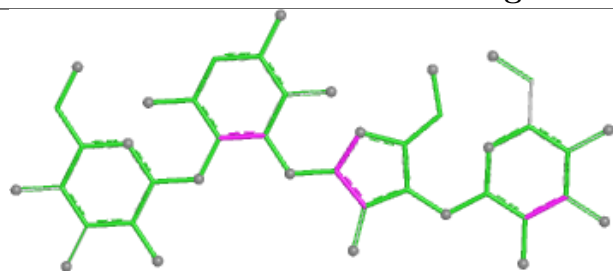


Torsions

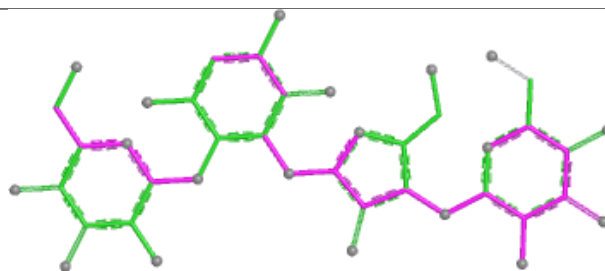


Rings

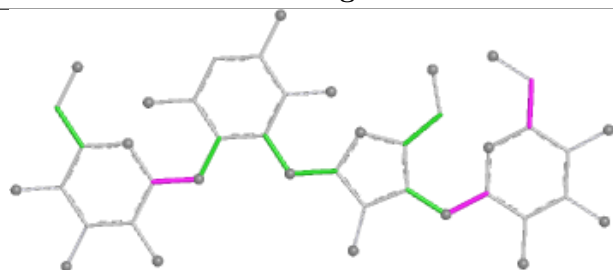
Ligand PAR A 1607



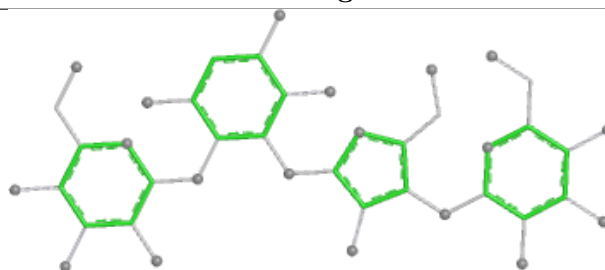
Bond lengths



Bond angles

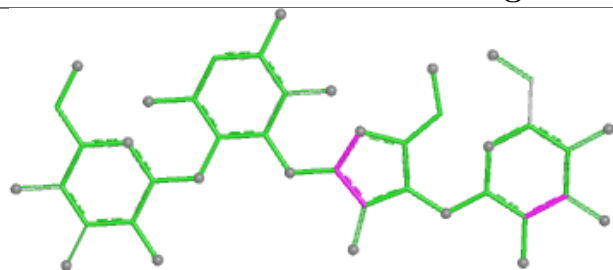


Torsions

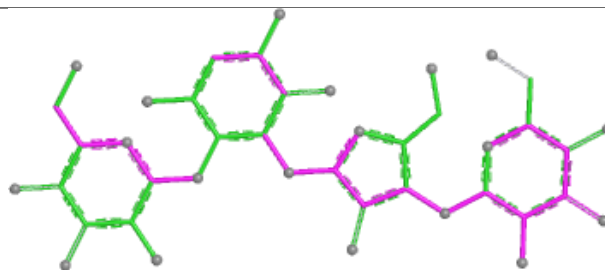


Rings

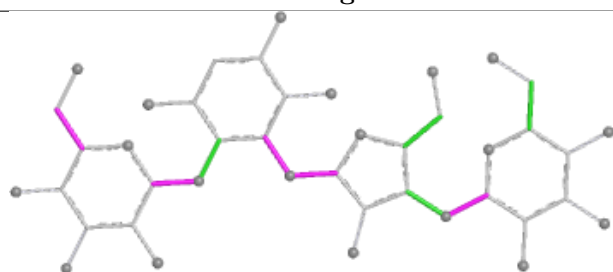
Ligand PAR A 1608



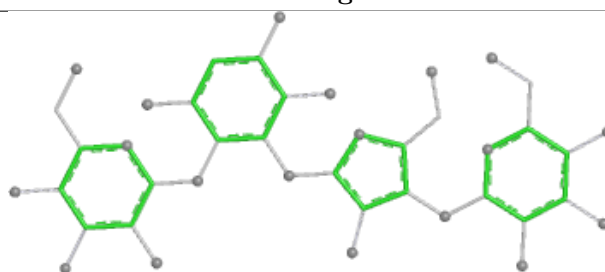
Bond lengths



Bond angles

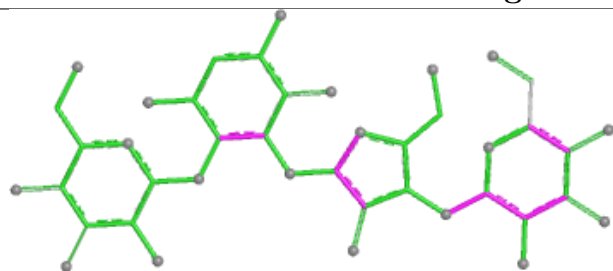


Torsions

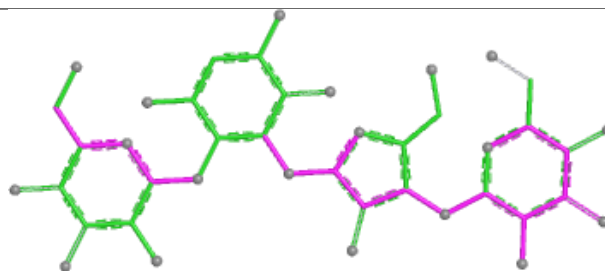


Rings

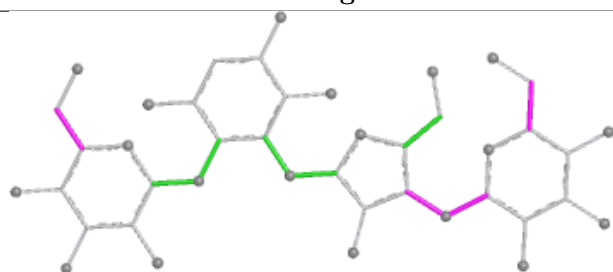
Ligand PAR A 1610



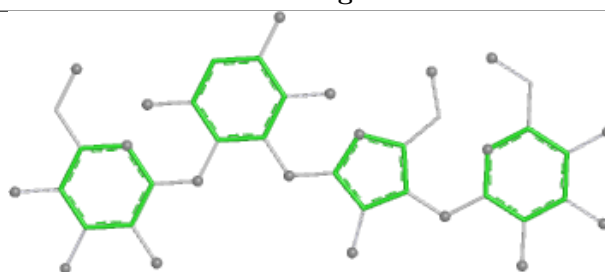
Bond lengths



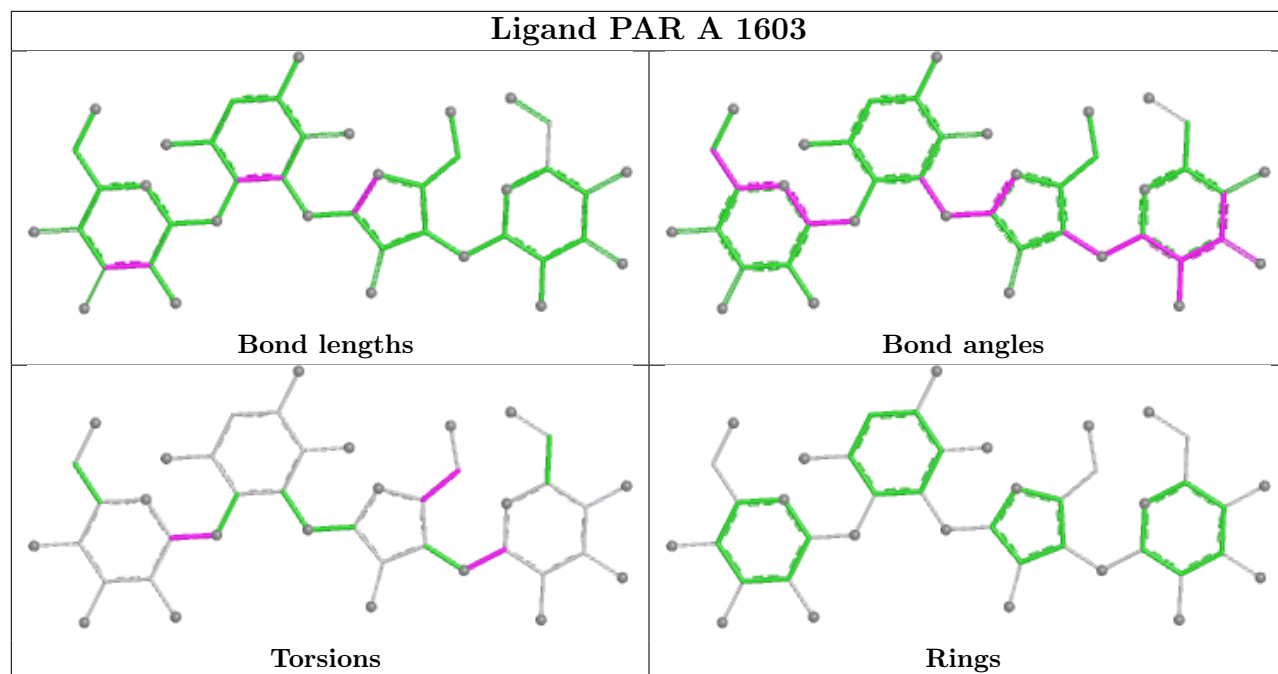
Bond angles



Torsions



Rings



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	A	1498/1522 (98%)	-0.39	49 (3%)	49	35	48, 80, 183, 551	0
2	B	236/256 (92%)	-0.15	3 (1%)	74	61	60, 104, 154, 168	0
3	C	207/239 (86%)	-0.01	5 (2%)	59	44	69, 106, 153, 184	0
4	D	208/209 (99%)	-0.13	8 (3%)	44	32	53, 86, 123, 147	0
5	E	151/162 (93%)	-0.57	0	100	100	50, 70, 105, 144	0
6	F	101/101 (100%)	-0.08	0	100	100	73, 111, 136, 155	0
7	G	155/156 (99%)	-0.14	4 (2%)	57	42	66, 100, 155, 187	0
8	H	138/138 (100%)	-0.63	1 (0%)	84	74	45, 68, 95, 127	0
9	I	127/128 (99%)	0.22	7 (5%)	32	23	67, 110, 140, 169	0
10	J	99/105 (94%)	0.71	10 (10%)	14	11	69, 133, 194, 209	0
11	K	117/129 (90%)	-0.27	2 (1%)	69	54	57, 85, 120, 137	0
12	L	124/135 (91%)	0.04	5 (4%)	43	31	46, 87, 123, 166	0
13	M	118/126 (93%)	0.08	5 (4%)	41	30	72, 106, 131, 151	0
14	N	60/61 (98%)	0.23	4 (6%)	25	18	76, 97, 143, 194	0
15	O	88/89 (98%)	-0.30	0	100	100	67, 87, 119, 163	0
16	P	84/88 (95%)	-0.28	0	100	100	61, 77, 109, 166	0
17	Q	101/105 (96%)	-0.32	2 (1%)	64	50	54, 74, 108, 154	0
18	R	73/88 (82%)	-0.40	1 (1%)	73	59	65, 87, 190, 221	0
19	S	81/93 (87%)	0.44	6 (7%)	22	16	93, 124, 165, 187	0
20	T	99/106 (93%)	0.02	6 (6%)	28	20	61, 85, 130, 156	0
21	U	25/27 (92%)	0.48	3 (12%)	10	8	77, 95, 129, 151	0
All	All	3890/4063 (95%)	-0.21	121 (3%)	51	37	45, 89, 156, 551	0

The worst 5 of 121 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1033	G	9.5
19	S	3	ARG	8.9
1	A	1129	C	7.8
1	A	1034	G	7.6
4	D	31	CYS	7.2

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	PSU	A	1540	20/21	0.82	0.24	197,257,265,266	0
1	PSU	A	1541	20/21	0.90	0.17	205,208,212,214	0
1	PSU	A	516	20/21	0.95	0.08	91,99,107,112	0
1	5MC	A	967	21/22	0.97	0.09	53,66,76,80	0
1	2MG	A	1207	24/25	0.97	0.07	84,91,99,100	0
1	5MC	A	1400	21/22	0.97	0.09	56,78,91,92	0
1	5MC	A	1407	21/22	0.97	0.09	58,69,78,82	0
1	7MG	A	527	24/25	0.97	0.09	60,65,76,80	0
1	M2G	A	966	25/26	0.97	0.07	65,74,83,93	0
12	0TD	L	92	10/11	0.97	0.11	47,89,101,397	0
1	MA6	A	1518	24/25	0.98	0.07	57,62,73,74	0
1	MA6	A	1519	24/25	0.98	0.10	50,57,68,73	0
1	5MC	A	1404	21/22	0.98	0.08	52,62,70,73	0
1	4OC	A	1402	22/23	0.98	0.07	56,67,76,80	0
1	UR3	A	1498	21/22	0.98	0.10	57,68,78,81	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
23	MG	A	1768	1/1	0.51	0.33	122,122,122,122	0
23	MG	A	1882	1/1	0.55	0.43	94,94,94,94	0
23	MG	A	1758	1/1	0.57	0.11	149,149,149,149	0
23	MG	A	1807	1/1	0.59	0.44	96,96,96,96	0
23	MG	A	1804	1/1	0.59	0.57	103,103,103,103	0
23	MG	A	1902	1/1	0.59	0.37	93,93,93,93	0
24	ZN	D	301	1/1	0.61	0.50	194,194,194,194	0
23	MG	A	1824	1/1	0.63	0.15	92,92,92,92	0
23	MG	A	1756	1/1	0.64	0.23	158,158,158,158	0
23	MG	A	1836	1/1	0.65	0.52	86,86,86,86	0
23	MG	A	1730	1/1	0.68	0.47	98,98,98,98	0
23	MG	A	1864	1/1	0.69	0.58	96,96,96,96	0
23	MG	A	1828	1/1	0.70	0.22	100,100,100,100	0
23	MG	O	101	1/1	0.72	0.12	104,104,104,104	0
23	MG	A	1909	1/1	0.72	0.23	91,91,91,91	0
23	MG	A	1852	1/1	0.73	0.14	65,65,65,65	0
23	MG	A	1889	1/1	0.73	0.39	92,92,92,92	0
23	MG	A	1693	1/1	0.73	0.12	129,129,129,129	0
23	MG	A	1819	1/1	0.74	0.47	96,96,96,96	0
23	MG	A	1637	1/1	0.74	0.28	90,90,90,90	0
23	MG	A	1714	1/1	0.74	0.15	115,115,115,115	0
23	MG	A	1915	1/1	0.75	0.27	101,101,101,101	0
23	MG	A	1883	1/1	0.75	0.16	68,68,68,68	0
22	PAR	A	1614	42/42	0.75	0.21	147,147,147,147	0
23	MG	A	1748	1/1	0.76	0.25	115,115,115,115	0
23	MG	A	1880	1/1	0.76	0.45	96,96,96,96	0
23	MG	A	1851	1/1	0.77	0.34	89,89,89,89	0
23	MG	A	1795	1/1	0.77	0.37	101,101,101,101	0
23	MG	A	1863	1/1	0.77	0.28	90,90,90,90	0
23	MG	A	1798	1/1	0.77	0.26	75,75,75,75	0
23	MG	A	1874	1/1	0.77	0.33	90,90,90,90	0
23	MG	N	102	1/1	0.77	0.29	76,76,76,76	0
23	MG	A	1767	1/1	0.77	0.12	113,113,113,113	0
23	MG	A	1783	1/1	0.77	0.32	132,132,132,132	0
23	MG	A	1881	1/1	0.78	0.39	102,102,102,102	0
23	MG	A	1718	1/1	0.78	0.34	89,89,89,89	0
23	MG	A	1808	1/1	0.78	0.29	93,93,93,93	0
22	PAR	A	1611	42/42	0.78	0.24	130,130,130,130	0
23	MG	A	1786	1/1	0.78	0.16	154,154,154,154	0
23	MG	A	1747	1/1	0.79	0.32	166,166,166,166	0
23	MG	A	1838	1/1	0.79	0.52	80,80,80,80	0
23	MG	A	1759	1/1	0.79	0.32	79,79,79,79	0
23	MG	A	1749	1/1	0.80	0.09	138,138,138,138	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
23	MG	A	1789	1/1	0.80	0.31	100,100,100,100	0
23	MG	A	1830	1/1	0.80	0.35	92,92,92,92	0
23	MG	A	1736	1/1	0.81	0.13	138,138,138,138	0
23	MG	A	1785	1/1	0.81	0.16	142,142,142,142	0
23	MG	A	1856	1/1	0.81	0.32	90,90,90,90	0
23	MG	A	1885	1/1	0.81	0.32	96,96,96,96	0
23	MG	A	1859[A]	1/1	0.81	1.14	59,59,59,59	1
23	MG	A	1899[A]	1/1	0.81	0.96	45,45,45,45	1
23	MG	A	1899[B]	1/1	0.81	0.96	45,45,45,45	1
23	MG	A	1859[B]	1/1	0.81	1.14	59,59,59,59	1
23	MG	A	1723	1/1	0.81	0.13	103,103,103,103	0
23	MG	A	1787	1/1	0.81	0.07	165,165,165,165	0
23	MG	A	1629	1/1	0.81	0.15	96,96,96,96	0
23	MG	A	1877	1/1	0.81	0.31	105,105,105,105	0
23	MG	A	1817	1/1	0.81	0.59	99,99,99,99	0
23	MG	A	1829	1/1	0.82	0.19	90,90,90,90	0
23	MG	A	1872	1/1	0.82	0.15	59,59,59,59	0
23	MG	A	1706	1/1	0.82	0.26	123,123,123,123	0
23	MG	D	302	1/1	0.82	0.12	112,112,112,112	0
23	MG	A	1679	1/1	0.82	0.17	73,73,73,73	0
23	MG	A	1641	1/1	0.82	0.12	92,92,92,92	0
23	MG	A	1703	1/1	0.82	0.17	85,85,85,85	0
22	PAR	A	1613	42/42	0.83	0.34	152,152,152,152	0
23	MG	A	1811	1/1	0.83	0.37	87,87,87,87	0
23	MG	A	1799	1/1	0.83	0.21	74,74,74,74	0
23	MG	A	1792	1/1	0.83	0.23	100,100,100,100	0
23	MG	Q	201	1/1	0.83	0.17	86,86,86,86	0
23	MG	A	1737	1/1	0.83	0.20	105,105,105,105	0
23	MG	A	1910	1/1	0.84	0.21	80,80,80,80	0
23	MG	A	1622	1/1	0.84	0.18	111,111,111,111	0
23	MG	A	1849	1/1	0.84	0.30	63,63,63,63	0
22	PAR	A	1615	42/42	0.84	0.24	169,169,169,169	0
23	MG	A	1823	1/1	0.84	0.39	82,82,82,82	0
23	MG	A	1866	1/1	0.84	0.50	83,83,83,83	0
23	MG	A	1744	1/1	0.84	0.12	99,99,99,99	0
23	MG	A	1844	1/1	0.85	0.26	71,71,71,71	0
23	MG	A	1722	1/1	0.85	0.09	100,100,100,100	0
23	MG	A	1814	1/1	0.85	0.30	85,85,85,85	0
23	MG	A	1762	1/1	0.85	0.14	127,127,127,127	0
23	MG	A	1826	1/1	0.85	0.32	82,82,82,82	0
23	MG	E	201	1/1	0.85	0.12	110,110,110,110	0
23	MG	A	1893	1/1	0.85	0.34	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
23	MG	A	1896	1/1	0.85	0.23	89,89,89,89	0
23	MG	A	1837	1/1	0.85	0.40	84,84,84,84	0
23	MG	A	1827	1/1	0.85	0.38	91,91,91,91	0
23	MG	A	1731	1/1	0.86	0.13	140,140,140,140	0
23	MG	A	1867	1/1	0.86	0.51	75,75,75,75	0
23	MG	A	1728	1/1	0.86	0.11	144,144,144,144	0
23	MG	A	1805	1/1	0.86	0.25	83,83,83,83	0
23	MG	A	1715	1/1	0.86	0.09	107,107,107,107	0
23	MG	A	1816	1/1	0.87	0.26	75,75,75,75	0
23	MG	A	1870	1/1	0.87	0.55	75,75,75,75	0
23	MG	A	1770	1/1	0.87	0.09	101,101,101,101	0
23	MG	A	1699	1/1	0.87	0.06	112,112,112,112	0
23	MG	A	1831	1/1	0.87	0.27	85,85,85,85	0
23	MG	A	1835	1/1	0.87	0.39	72,72,72,72	0
23	MG	A	1742	1/1	0.87	0.13	146,146,146,146	0
23	MG	A	1919	1/1	0.87	0.25	85,85,85,85	0
23	MG	A	1861	1/1	0.87	0.38	75,75,75,75	0
23	MG	A	1862	1/1	0.87	0.41	70,70,70,70	0
23	MG	A	1630	1/1	0.87	0.14	87,87,87,87	0
23	MG	A	1886	1/1	0.87	0.31	86,86,86,86	0
23	MG	A	1698	1/1	0.87	0.19	91,91,91,91	0
23	MG	T	201	1/1	0.87	0.24	100,100,100,100	0
23	MG	A	1800	1/1	0.87	0.32	83,83,83,83	0
23	MG	A	1796	1/1	0.88	0.45	94,94,94,94	0
23	MG	A	1857	1/1	0.88	0.33	59,59,59,59	0
23	MG	A	1905	1/1	0.88	0.34	100,100,100,100	0
23	MG	A	1825	1/1	0.88	0.12	88,88,88,88	0
23	MG	A	1710	1/1	0.88	0.21	92,92,92,92	0
23	MG	A	1913	1/1	0.88	0.27	69,69,69,69	0
23	MG	A	1777	1/1	0.88	0.18	84,84,84,84	0
23	MG	A	1842	1/1	0.88	0.25	70,70,70,70	0
23	MG	A	1922	1/1	0.88	0.22	77,77,77,77	0
23	MG	A	1843	1/1	0.88	0.13	62,62,62,62	0
23	MG	A	1733	1/1	0.88	0.08	142,142,142,142	0
23	MG	A	1888	1/1	0.88	0.31	71,71,71,71	0
23	MG	A	1846	1/1	0.88	0.48	81,81,81,81	0
23	MG	A	1791	1/1	0.88	0.28	84,84,84,84	0
23	MG	S	101	1/1	0.88	0.18	83,83,83,83	0
23	MG	A	1784	1/1	0.88	0.12	127,127,127,127	0
23	MG	A	1628	1/1	0.88	0.15	44,44,44,44	0
22	PAR	A	1616	42/42	0.89	0.23	126,126,126,126	42
23	MG	A	1797	1/1	0.89	0.37	85,85,85,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
23	MG	A	1700	1/1	0.89	0.28	90,90,90,90	0
23	MG	A	1865	1/1	0.89	0.15	66,66,66,66	0
23	MG	A	1918	1/1	0.89	0.29	90,90,90,90	0
22	PAR	A	1617	42/42	0.89	0.23	137,137,137,137	0
23	MG	A	1921[A]	1/1	0.89	0.30	28,28,28,28	1
23	MG	A	1921[B]	1/1	0.89	0.30	28,28,28,28	1
23	MG	A	1788	1/1	0.89	0.44	75,75,75,75	0
23	MG	A	1854	1/1	0.89	0.21	76,76,76,76	0
23	MG	A	1802	1/1	0.89	0.19	71,71,71,71	0
23	MG	F	201	1/1	0.89	0.35	80,80,80,80	0
23	MG	A	1750	1/1	0.89	0.17	100,100,100,100	0
23	MG	A	1717	1/1	0.89	0.21	110,110,110,110	0
23	MG	A	1900	1/1	0.89	0.20	77,77,77,77	0
23	MG	A	1743	1/1	0.89	0.09	145,145,145,145	0
23	MG	A	1649	1/1	0.89	0.10	90,90,90,90	0
23	MG	A	1907	1/1	0.89	0.20	81,81,81,81	0
23	MG	A	1692	1/1	0.90	0.08	98,98,98,98	0
23	MG	A	1916[A]	1/1	0.90	0.42	50,50,50,50	1
23	MG	A	1916[B]	1/1	0.90	0.42	50,50,50,50	1
23	MG	A	1753	1/1	0.90	0.10	109,109,109,109	0
23	MG	A	1850	1/1	0.90	0.20	60,60,60,60	0
22	PAR	A	1610	42/42	0.90	0.18	111,111,111,111	0
23	MG	A	1740	1/1	0.90	0.14	96,96,96,96	0
23	MG	A	1725	1/1	0.90	0.07	94,94,94,94	0
23	MG	A	1822	1/1	0.90	0.28	69,69,69,69	0
23	MG	A	1726	1/1	0.90	0.11	91,91,91,91	0
23	MG	A	1652	1/1	0.90	0.31	86,86,86,86	0
23	MG	A	1879	1/1	0.90	0.34	79,79,79,79	0
23	MG	A	1656	1/1	0.90	0.18	124,124,124,124	0
23	MG	A	1860	1/1	0.90	0.51	102,102,102,102	0
23	MG	A	1621	1/1	0.90	0.12	131,131,131,131	0
23	MG	A	1691	1/1	0.90	0.25	118,118,118,118	0
23	MG	A	1884	1/1	0.90	0.33	85,85,85,85	0
23	MG	A	1813	1/1	0.91	0.11	55,55,55,55	0
23	MG	A	1920	1/1	0.91	0.14	72,72,72,72	0
23	MG	A	1704	1/1	0.91	0.10	87,87,87,87	0
23	MG	A	1790	1/1	0.91	0.26	89,89,89,89	0
23	MG	A	1683	1/1	0.91	0.14	73,73,73,73	0
23	MG	A	1620	1/1	0.91	0.18	91,91,91,91	0
23	MG	A	1832	1/1	0.91	0.26	68,68,68,68	0
23	MG	E	202	1/1	0.91	0.28	74,74,74,74	0
23	MG	A	1766	1/1	0.91	0.08	118,118,118,118	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
23	MG	A	1670	1/1	0.91	0.20	84,84,84,84	0
23	MG	A	1887	1/1	0.91	0.41	93,93,93,93	0
22	PAR	A	1605	42/42	0.91	0.16	93,93,93,93	0
23	MG	A	1809	1/1	0.91	0.22	58,58,58,58	0
23	MG	A	1841	1/1	0.91	0.14	74,74,74,74	0
23	MG	A	1735	1/1	0.91	0.16	92,92,92,92	0
23	MG	A	1820	1/1	0.92	0.29	88,88,88,88	0
23	MG	A	1775	1/1	0.92	0.12	83,83,83,83	0
23	MG	A	1694	1/1	0.92	0.11	97,97,97,97	0
23	MG	A	1671	1/1	0.92	0.18	68,68,68,68	0
23	MG	A	1678	1/1	0.92	0.11	101,101,101,101	0
23	MG	A	1643	1/1	0.92	0.34	74,74,74,74	0
23	MG	A	1754	1/1	0.92	0.09	111,111,111,111	0
23	MG	A	1917	1/1	0.92	0.47	68,68,68,68	0
23	MG	A	1806	1/1	0.92	0.23	81,81,81,81	0
23	MG	A	1635	1/1	0.92	0.19	65,65,65,65	0
23	MG	A	1738	1/1	0.92	0.21	116,116,116,116	0
22	PAR	A	1612	42/42	0.92	0.16	69,69,69,69	42
23	MG	A	1761	1/1	0.92	0.11	103,103,103,103	0
23	MG	A	1833	1/1	0.92	0.24	58,58,58,58	0
23	MG	A	1834	1/1	0.92	0.26	77,77,77,77	0
23	MG	A	1812	1/1	0.92	0.35	77,77,77,77	0
23	MG	A	1895[A]	1/1	0.92	0.38	30,30,30,30	1
23	MG	A	1895[B]	1/1	0.92	0.38	30,30,30,30	1
23	MG	I	201	1/1	0.92	0.18	92,92,92,92	0
23	MG	L	201	1/1	0.92	0.17	81,81,81,81	0
23	MG	A	1741	1/1	0.92	0.15	76,76,76,76	0
23	MG	A	1640	1/1	0.92	0.18	78,78,78,78	0
23	MG	A	1709	1/1	0.92	0.32	87,87,87,87	0
23	MG	A	1840	1/1	0.92	0.19	79,79,79,79	0
22	PAR	A	1607	42/42	0.92	0.16	92,92,92,92	42
23	MG	T	202	1/1	0.92	0.34	56,56,56,56	0
23	MG	A	1713	1/1	0.92	0.10	95,95,95,95	0
23	MG	A	1664	1/1	0.93	0.15	94,94,94,94	0
22	PAR	A	1608	42/42	0.93	0.17	97,97,97,97	0
23	MG	A	1755	1/1	0.93	0.14	96,96,96,96	0
22	PAR	A	1603	42/42	0.93	0.13	83,83,83,83	3
23	MG	A	1914	1/1	0.93	0.49	81,81,81,81	0
23	MG	A	1674	1/1	0.93	0.14	96,96,96,96	0
23	MG	A	1878	1/1	0.93	0.19	49,49,49,49	0
23	MG	A	1651	1/1	0.93	0.44	61,61,61,61	0
23	MG	A	1739	1/1	0.93	0.31	84,84,84,84	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
23	MG	A	1845	1/1	0.93	0.15	63,63,63,63	0
23	MG	A	1720	1/1	0.93	0.08	94,94,94,94	0
23	MG	A	1821	1/1	0.93	0.26	82,82,82,82	0
23	MG	A	1793	1/1	0.93	0.51	84,84,84,84	0
23	MG	A	1763	1/1	0.93	0.16	102,102,102,102	0
23	MG	A	1624	1/1	0.93	0.09	95,95,95,95	0
23	MG	A	1680	1/1	0.93	0.09	85,85,85,85	0
23	MG	A	1682	1/1	0.93	0.10	33,33,33,33	0
23	MG	A	1653	1/1	0.93	0.09	96,96,96,96	0
23	MG	A	1773	1/1	0.93	0.16	91,91,91,91	0
23	MG	A	1801	1/1	0.93	0.49	87,87,87,87	0
23	MG	A	1774	1/1	0.93	0.14	95,95,95,95	0
23	MG	A	1727	1/1	0.93	0.09	117,117,117,117	0
23	MG	A	1707	1/1	0.93	0.10	112,112,112,112	0
23	MG	A	1778	1/1	0.93	0.14	107,107,107,107	0
23	MG	A	1781	1/1	0.93	0.09	104,104,104,104	0
23	MG	A	1687	1/1	0.93	0.10	92,92,92,92	0
23	MG	A	1904	1/1	0.93	0.15	80,80,80,80	0
23	MG	A	1632	1/1	0.93	0.08	68,68,68,68	0
23	MG	A	1645	1/1	0.94	0.17	64,64,64,64	0
23	MG	A	1676	1/1	0.94	0.10	82,82,82,82	0
23	MG	A	1654	1/1	0.94	0.11	104,104,104,104	0
23	MG	A	1906	1/1	0.94	0.14	75,75,75,75	0
23	MG	A	1839	1/1	0.94	0.24	84,84,84,84	0
23	MG	A	1868	1/1	0.94	0.33	73,73,73,73	0
23	MG	A	1655	1/1	0.94	0.08	87,87,87,87	0
23	MG	A	1871	1/1	0.94	0.38	85,85,85,85	0
22	PAR	A	1606	42/42	0.94	0.11	64,64,64,64	42
23	MG	A	1818	1/1	0.94	0.24	79,79,79,79	0
23	MG	A	1721	1/1	0.94	0.11	93,93,93,93	0
23	MG	A	1769	1/1	0.94	0.06	108,108,108,108	0
23	MG	A	1650	1/1	0.94	0.09	106,106,106,106	0
23	MG	A	1701	1/1	0.94	0.16	83,83,83,83	0
23	MG	A	1848	1/1	0.94	0.42	71,71,71,71	0
23	MG	A	1745	1/1	0.94	0.12	79,79,79,79	0
23	MG	A	1669	1/1	0.94	0.10	76,76,76,76	0
23	MG	A	1684	1/1	0.94	0.12	81,81,81,81	0
23	MG	A	1685	1/1	0.94	0.26	90,90,90,90	0
23	MG	A	1853	1/1	0.94	0.19	55,55,55,55	0
23	MG	A	1803	1/1	0.94	0.24	62,62,62,62	0
23	MG	A	1855	1/1	0.94	0.26	74,74,74,74	0
23	MG	A	1686	1/1	0.94	0.08	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
23	MG	H	201	1/1	0.94	0.07	85,85,85,85	0
23	MG	A	1890	1/1	0.94	0.21	86,86,86,86	0
23	MG	A	1708	1/1	0.94	0.10	77,77,77,77	0
23	MG	A	1638	1/1	0.94	0.19	93,93,93,93	0
23	MG	A	1732	1/1	0.94	0.20	86,86,86,86	0
23	MG	A	1689	1/1	0.94	0.11	87,87,87,87	0
23	MG	A	1897	1/1	0.94	0.14	47,47,47,47	0
23	MG	A	1712	1/1	0.94	0.07	112,112,112,112	0
23	MG	A	1810	1/1	0.94	0.18	63,63,63,63	0
23	MG	A	1639	1/1	0.94	0.20	72,72,72,72	0
23	MG	A	1663	1/1	0.95	0.17	92,92,92,92	0
23	MG	A	1677	1/1	0.95	0.08	70,70,70,70	0
22	PAR	A	1602	42/42	0.95	0.10	58,58,58,58	0
23	MG	A	1688	1/1	0.95	0.19	115,115,115,115	0
23	MG	A	1892	1/1	0.95	0.12	58,58,58,58	0
23	MG	A	1869	1/1	0.95	0.34	71,71,71,71	0
23	MG	A	1894	1/1	0.95	0.25	64,64,64,64	0
23	MG	A	1667	1/1	0.95	0.09	78,78,78,78	0
23	MG	A	1794	1/1	0.95	0.25	80,80,80,80	0
23	MG	A	1760	1/1	0.95	0.15	77,77,77,77	0
22	PAR	A	1609	42/42	0.95	0.13	77,77,77,77	42
23	MG	A	1876	1/1	0.95	0.14	60,60,60,60	0
23	MG	A	1746	1/1	0.95	0.12	88,88,88,88	0
23	MG	A	1858[A]	1/1	0.95	0.70	32,32,32,32	1
23	MG	A	1901	1/1	0.95	0.28	81,81,81,81	0
23	MG	A	1858[B]	1/1	0.95	0.70	32,32,32,32	1
23	MG	H	202	1/1	0.95	0.11	72,72,72,72	0
23	MG	A	1681	1/1	0.95	0.08	89,89,89,89	0
22	PAR	A	1601	42/42	0.95	0.11	70,70,70,70	0
22	PAR	A	1604	42/42	0.95	0.12	70,70,70,70	0
23	MG	A	1815	1/1	0.95	0.08	71,71,71,71	0
23	MG	A	1908	1/1	0.95	0.19	69,69,69,69	0
23	MG	A	1697	1/1	0.95	0.39	66,66,66,66	0
23	MG	A	1847	1/1	0.95	0.30	70,70,70,70	0
23	MG	A	1912	1/1	0.95	0.12	70,70,70,70	0
23	MG	A	1642	1/1	0.95	0.08	77,77,77,77	0
23	MG	A	1751	1/1	0.96	0.13	81,81,81,81	0
23	MG	A	1752	1/1	0.96	0.09	105,105,105,105	0
23	MG	A	1661	1/1	0.96	0.16	112,112,112,112	0
23	MG	A	1716	1/1	0.96	0.06	74,74,74,74	0
23	MG	A	1627	1/1	0.96	0.08	70,70,70,70	0
23	MG	A	1636	1/1	0.96	0.10	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
23	MG	A	1675	1/1	0.96	0.09	101,101,101,101	0
23	MG	A	1690	1/1	0.96	0.08	108,108,108,108	0
23	MG	A	1873	1/1	0.96	0.33	59,59,59,59	0
23	MG	A	1911	1/1	0.96	0.20	62,62,62,62	0
23	MG	A	1711	1/1	0.96	0.16	102,102,102,102	0
23	MG	A	1875	1/1	0.96	0.11	55,55,55,55	0
23	MG	A	1779	1/1	0.96	0.12	70,70,70,70	0
23	MG	A	1780	1/1	0.96	0.07	66,66,66,66	0
23	MG	P	101	1/1	0.96	0.22	63,63,63,63	0
23	MG	A	1646	1/1	0.96	0.12	85,85,85,85	0
23	MG	A	1724	1/1	0.96	0.05	97,97,97,97	0
23	MG	A	1668	1/1	0.96	0.08	92,92,92,92	0
23	MG	A	1765	1/1	0.96	0.10	107,107,107,107	0
23	MG	A	1647	1/1	0.96	0.14	101,101,101,101	0
23	MG	A	1644	1/1	0.97	0.05	50,50,50,50	0
23	MG	A	1702	1/1	0.97	0.08	68,68,68,68	0
23	MG	A	1757	1/1	0.97	0.16	61,61,61,61	0
23	MG	A	1771	1/1	0.97	0.05	67,67,67,67	0
23	MG	A	1903	1/1	0.97	0.06	46,46,46,46	0
23	MG	A	1619	1/1	0.97	0.06	79,79,79,79	0
23	MG	A	1673	1/1	0.97	0.07	70,70,70,70	0
23	MG	A	1696	1/1	0.97	0.06	84,84,84,84	0
23	MG	A	1618	1/1	0.97	0.14	79,79,79,79	0
23	MG	A	1634	1/1	0.97	0.07	44,44,44,44	0
23	MG	A	1658	1/1	0.97	0.07	103,103,103,103	0
23	MG	A	1729	1/1	0.97	0.09	93,93,93,93	0
23	MG	A	1719	1/1	0.97	0.12	71,71,71,71	0
23	MG	A	1660	1/1	0.97	0.05	66,66,66,66	0
23	MG	A	1666	1/1	0.98	0.05	54,54,54,54	0
23	MG	A	1659	1/1	0.98	0.05	84,84,84,84	0
23	MG	A	1782	1/1	0.98	0.10	62,62,62,62	0
23	MG	A	1633	1/1	0.98	0.06	64,64,64,64	0
23	MG	A	1631	1/1	0.98	0.05	78,78,78,78	0
23	MG	A	1891	1/1	0.98	0.50	70,70,70,70	0
23	MG	A	1657	1/1	0.98	0.06	54,54,54,54	0
23	MG	A	1625	1/1	0.98	0.08	90,90,90,90	0
23	MG	A	1705	1/1	0.98	0.07	76,76,76,76	0
23	MG	A	1672	1/1	0.98	0.05	58,58,58,58	0
23	MG	A	1764	1/1	0.98	0.12	107,107,107,107	0
23	MG	A	1734	1/1	0.98	0.08	96,96,96,96	0
23	MG	A	1665	1/1	0.98	0.04	90,90,90,90	0
23	MG	A	1898	1/1	0.98	0.15	55,55,55,55	0

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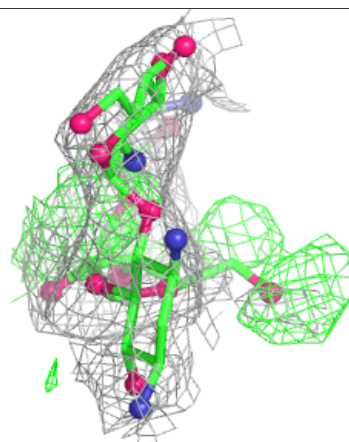
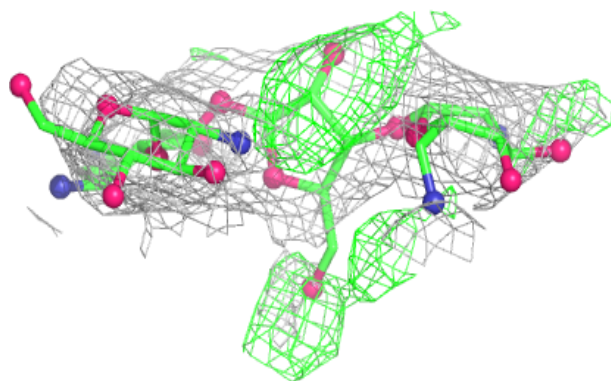
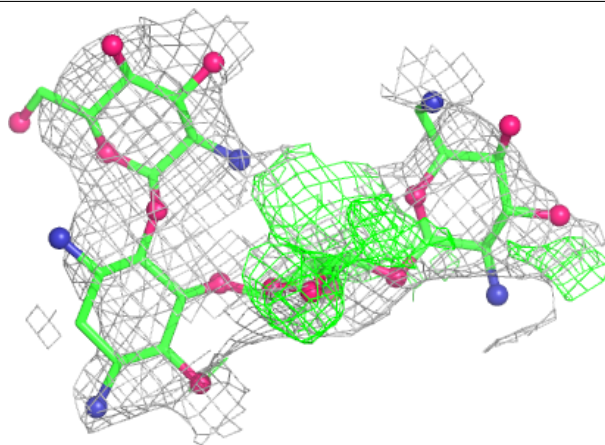
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
23	MG	D	303	1/1	0.98	0.08	63,63,63,63	0
23	MG	A	1623	1/1	0.99	0.07	62,62,62,62	0
23	MG	A	1772	1/1	0.99	0.06	67,67,67,67	0
23	MG	A	1648	1/1	0.99	0.05	86,86,86,86	0
23	MG	A	1626	1/1	0.99	0.09	53,53,53,53	0
23	MG	A	1662	1/1	0.99	0.16	59,59,59,59	0
23	MG	A	1776	1/1	0.99	0.11	86,86,86,86	0
23	MG	A	1695	1/1	0.99	0.04	62,62,62,62	0
24	ZN	N	101	1/1	0.99	0.10	141,141,141,141	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

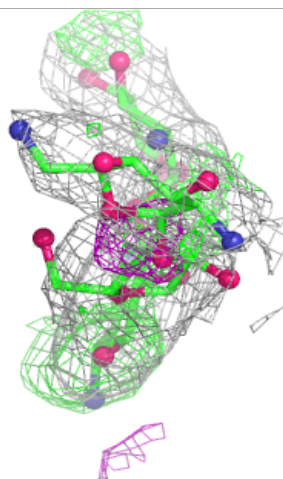
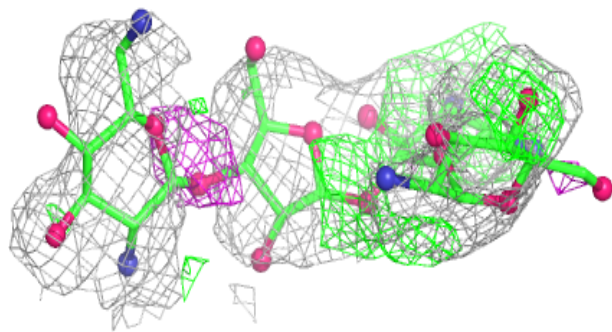
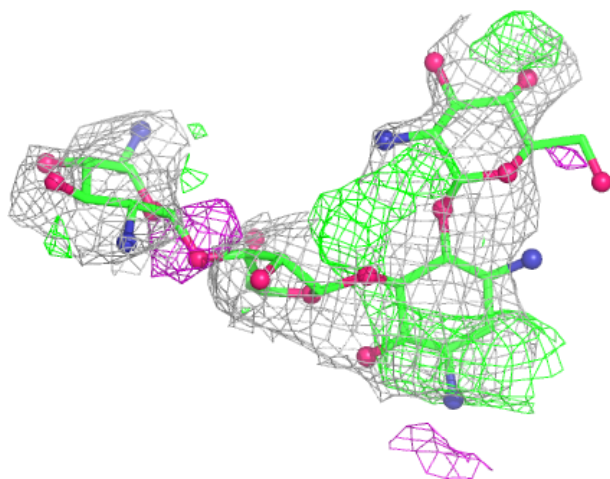
Electron density around PAR A 1614:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



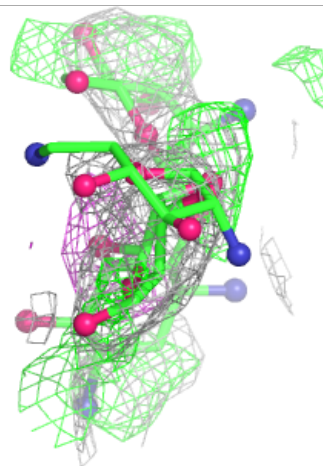
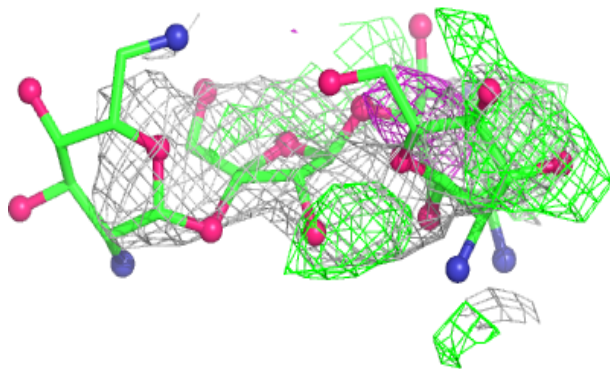
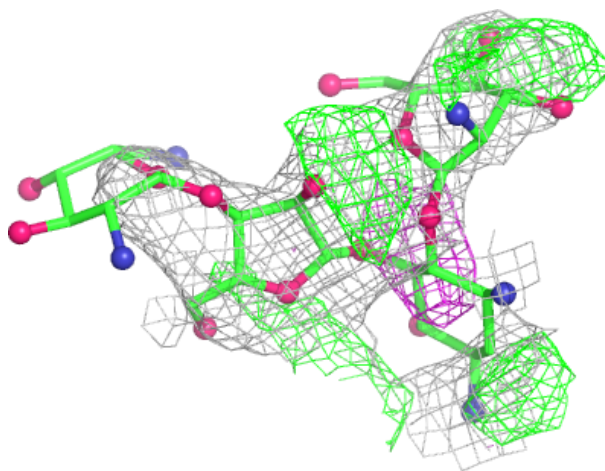
Electron density around PAR A 1611:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



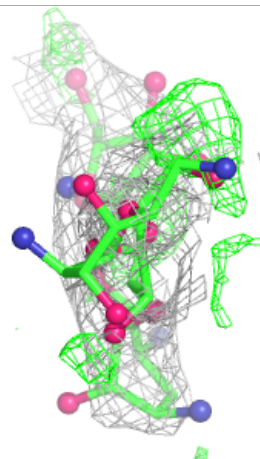
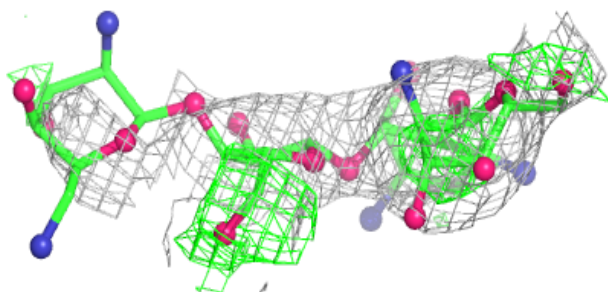
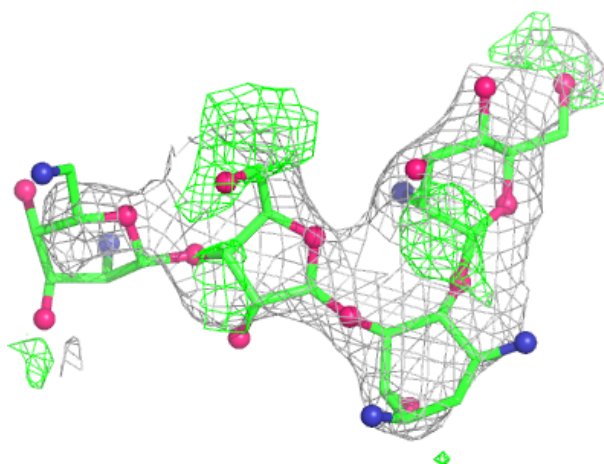
Electron density around PAR A 1613:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



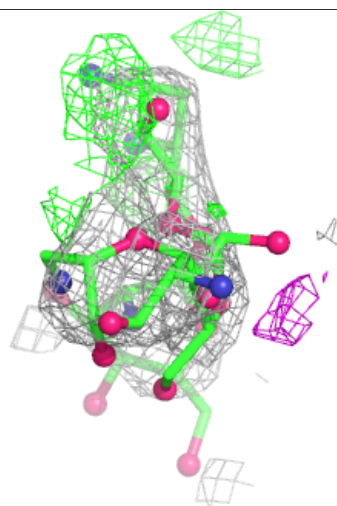
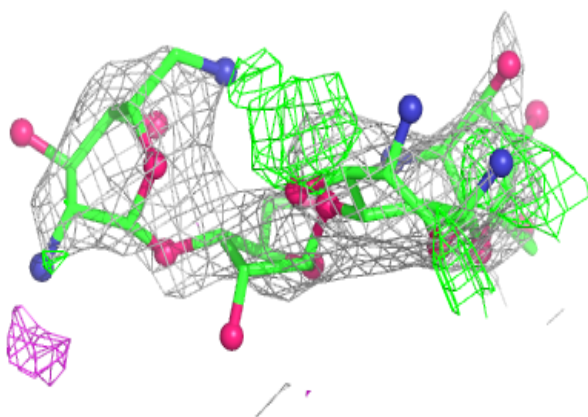
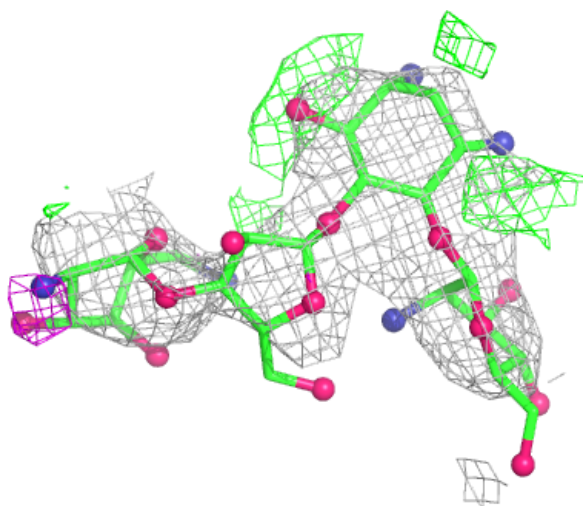
Electron density around PAR A 1615:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



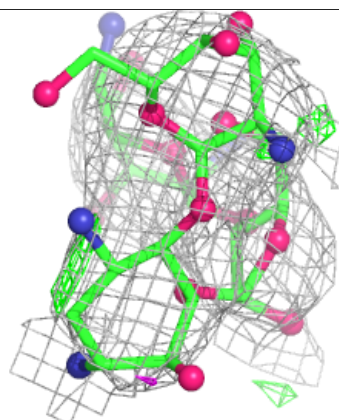
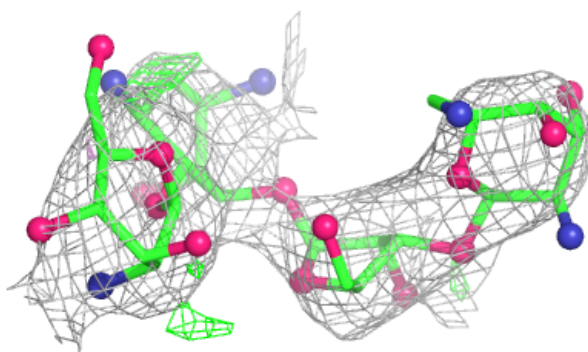
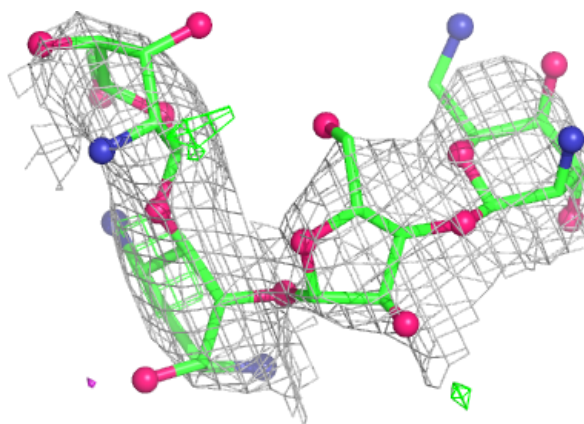
Electron density around PAR A 1616:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



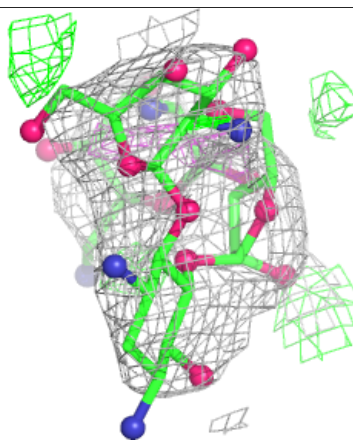
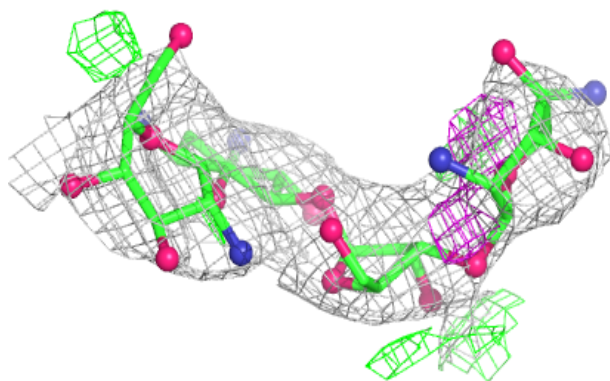
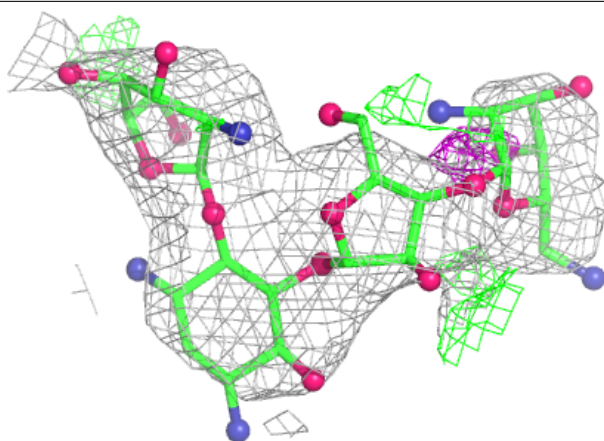
Electron density around PAR A 1617:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



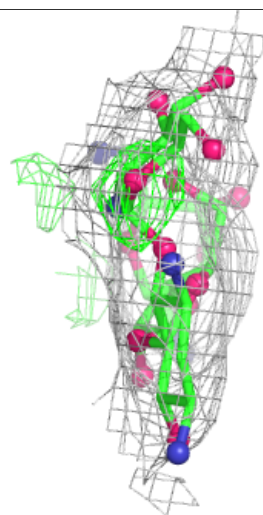
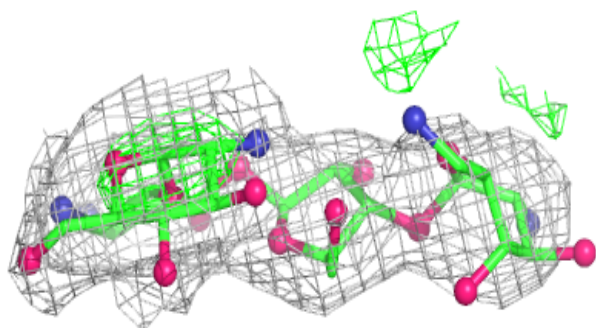
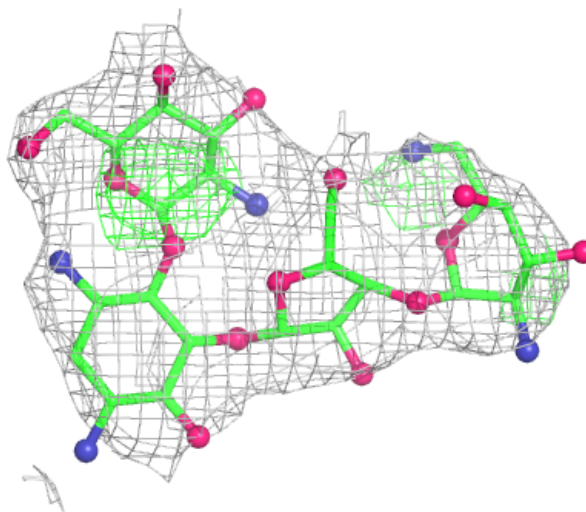
Electron density around PAR A 1610:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



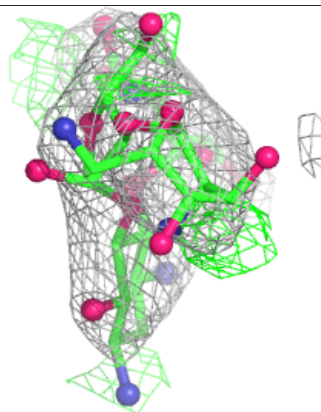
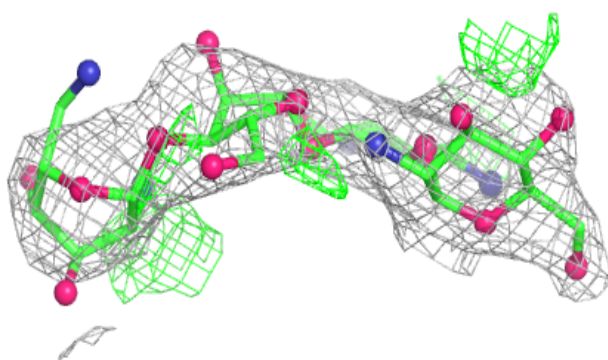
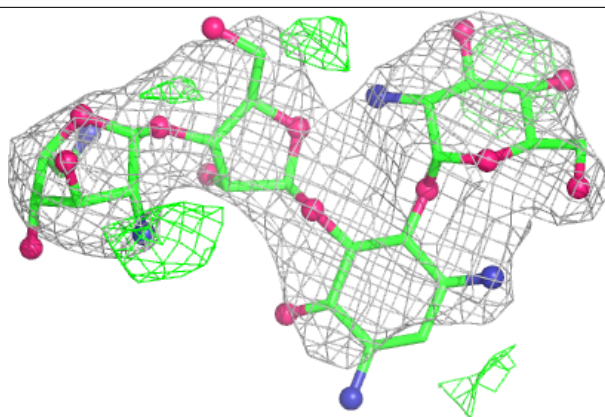
Electron density around PAR A 1605:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



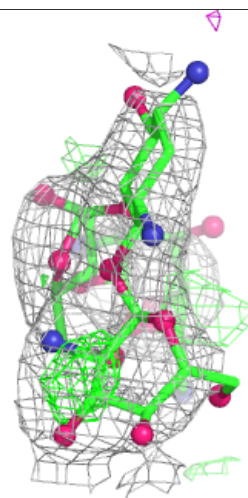
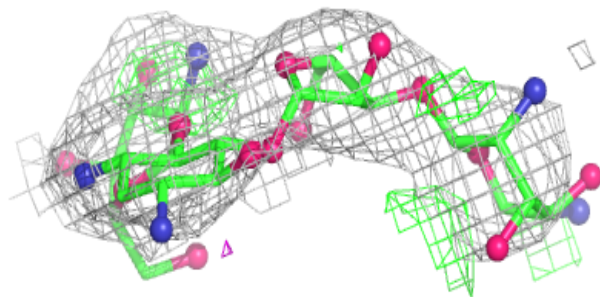
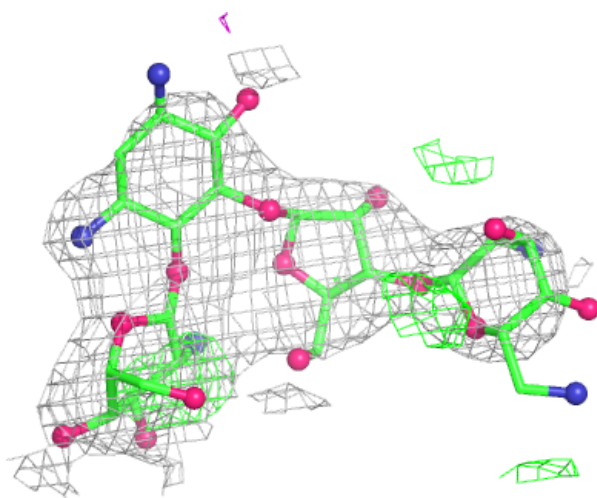
Electron density around PAR A 1612:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



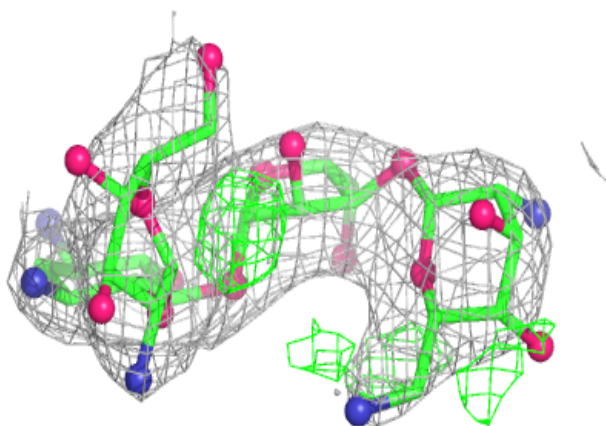
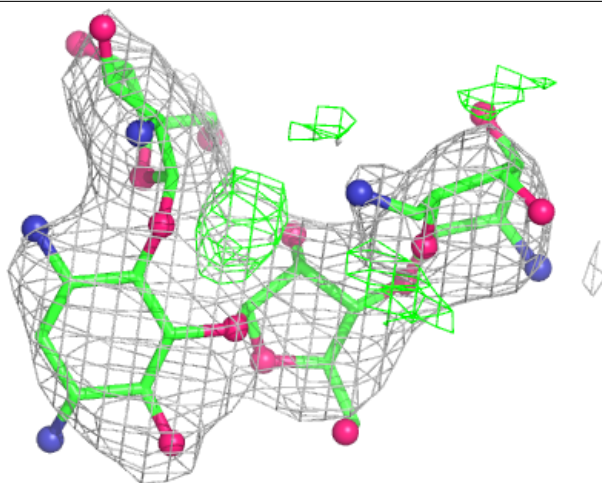
Electron density around PAR A 1607:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



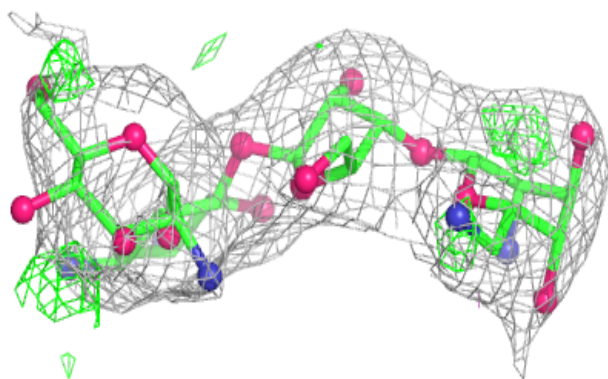
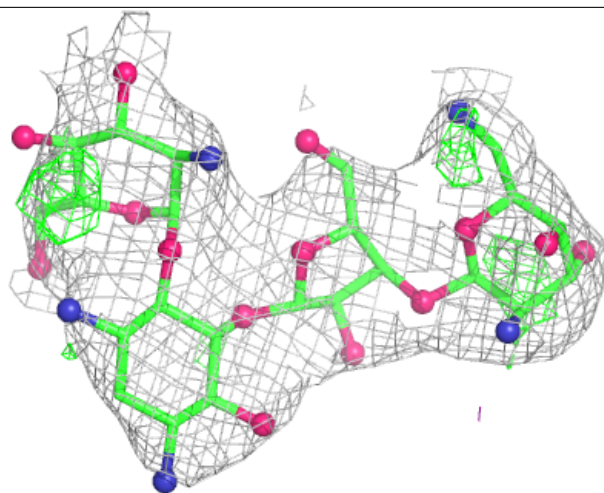
Electron density around PAR A 1608:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



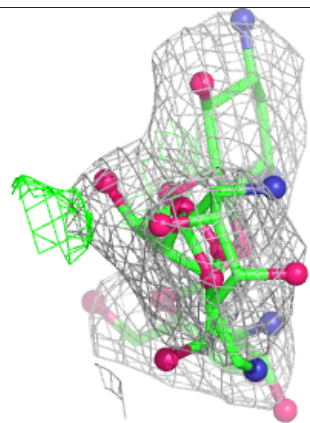
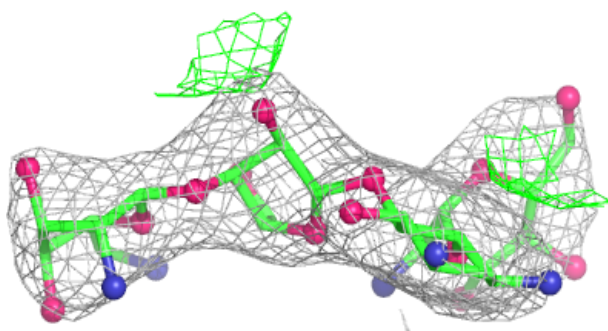
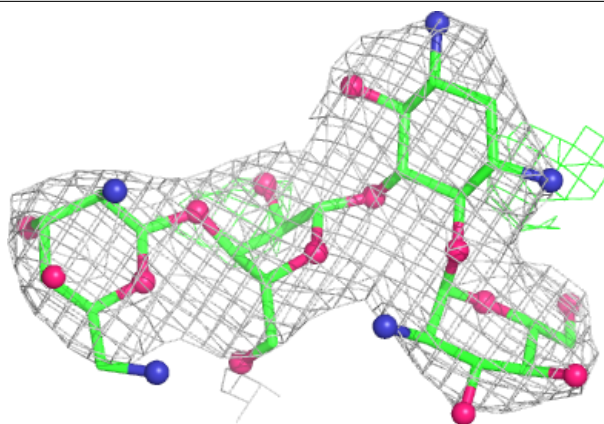
Electron density around PAR A 1603:

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and green (positive)



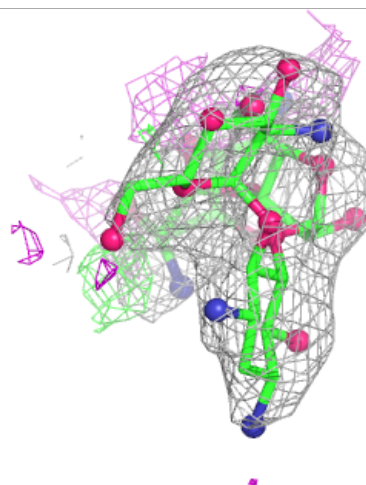
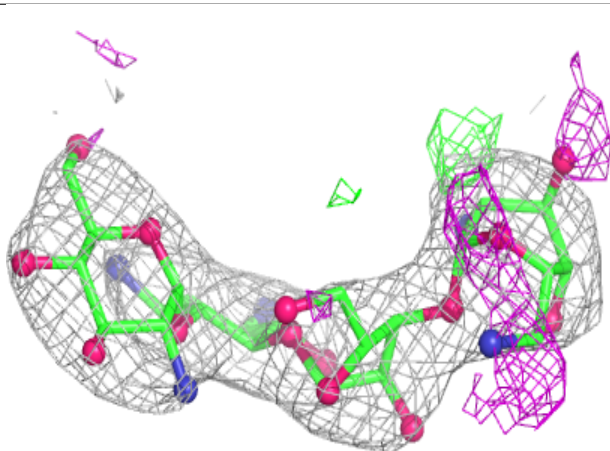
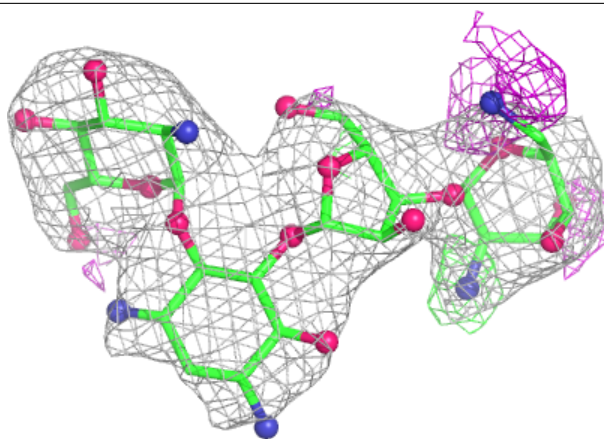
Electron density around PAR A 1606:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



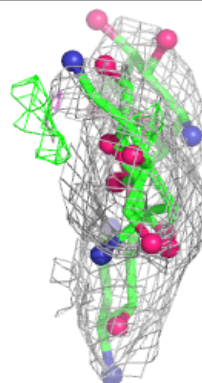
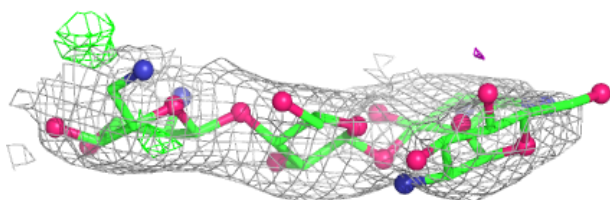
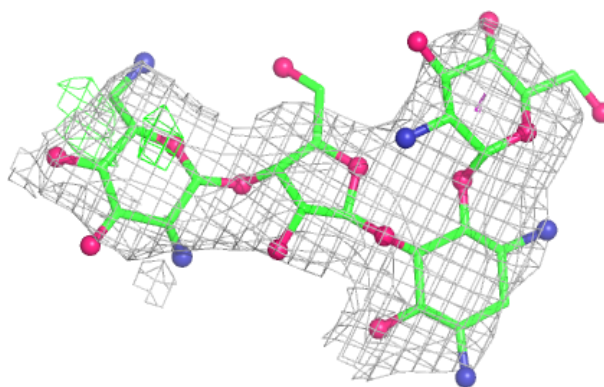
Electron density around PAR A 1602:

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and green (positive)

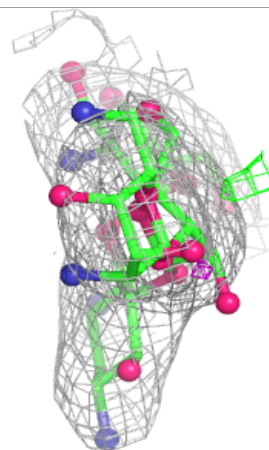
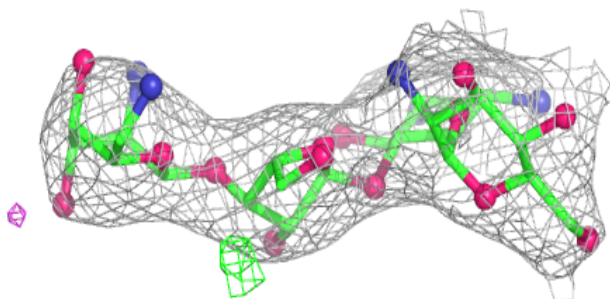
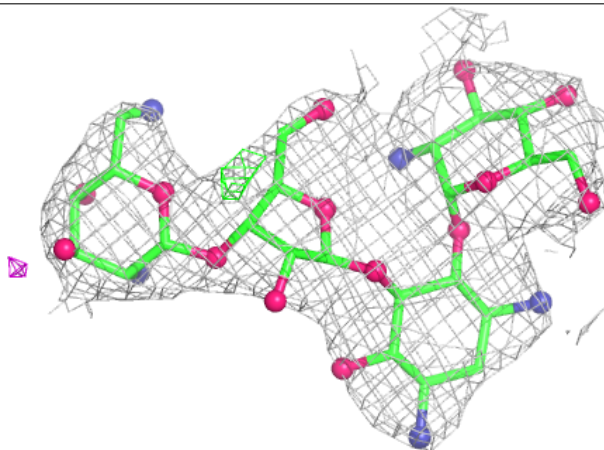


Electron density around PAR A 1609:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

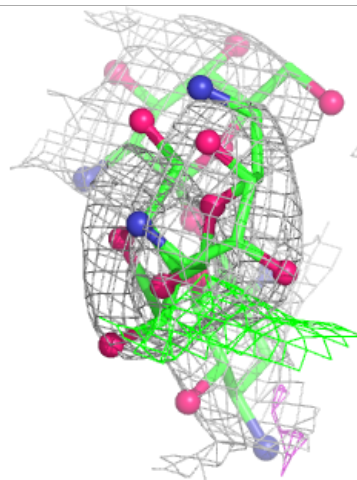
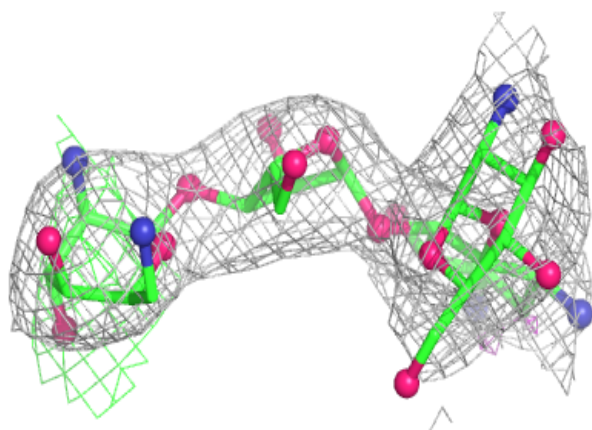
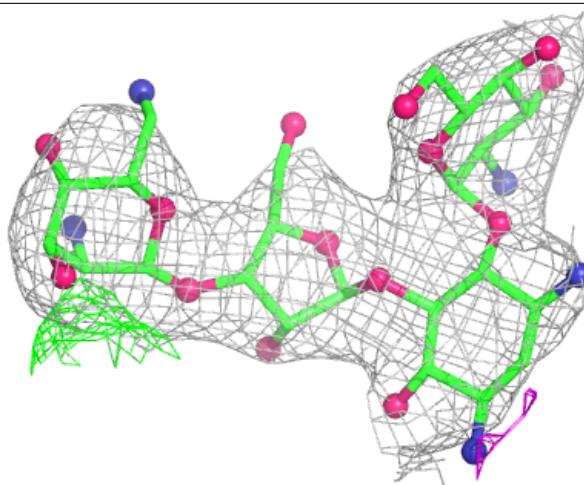
**Electron density around PAR A 1601:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around PAR A 1604:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.